1 DT12 Rec'd PCT/PTO 2 9 NOV 2004

SEQUENCE LISTING

SEQUENCE DISTING	
<110> SunGene GmbH & Co.KGaA	
<120> Method for achieving a pathogen resistance in plants	
<130> PF53687	
<140> <141>	
<160> 36	
<170> PatentIn Ver. 2.1	
<210> 1 <211> 1890 <212> DNA <213> Protaminobacter rubrum	
<220> <221> CDS <222> (1)(1887) <223> coding for sucrose isomerase	
<400> 1	
atg ccc cgt caa gga ttg aaa act gca cta gcg att ttt cta acc aca 48 Met Pro Arg Gln Gly Leu Lys Thr Ala Leu Ala Ile Phe Leu Thr Thr 1 5 10 15	8
tca tta tgc atc tca tgc cag caa gcc ttc ggt acg caa caa ccc ttg 96 Ser Leu Cys Ile Ser Cys Gln Gln Ala Phe Gly Thr Gln Gln Pro Leu 20 25 30	6
ctt aac gaa aag agt atc gaa cag tcg aaa acc ata cct aaa tgg tgg 14 Leu Asn Glu Lys Ser Ile Glu Gln Ser Lys Thr Ile Pro Lys Trp Trp 35 40 45	44
aag gag gct gtt ttt tat cag gtg tat ccg cgc tcc ttt aaa gac acc 19 Lys Glu Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr 50 55 60	92
aac gga gat ggc atc ggg gat att aac ggc atc ata gaa aaa tta gac 24 Asn Gly Asp Gly Ile Gly Asp Ile Asn Gly Ile Ile Glu Lys Leu Asp 65 70 .75 80	40
tat cta aaa gcc ttg ggg att gat gcc att tgg atc aac cca cat tat 28 Tyr Leu Lys Ala Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr 85 90 95	88
gat tot ccg aac acg gat aat ggt tac gat ata cgt gat tat cga aaa 33 Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys 100 105 110	36
atc atg aaa gaa tat ggc acg atg gag gat ttt gac cgc ctg att tct 38 Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser 115 120 125	84
gaa atg aaa aaa cgg aat atg cgg ttg atg att gat gtg gtc atc aac 43 Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn 130 135 140	32 ,
cac acc agc gat caa aac gaa tgg ttt gtt aaa agt aaa agc agt aag 48 His Thr Ser Asp Gln Asn Glu Trp Phe Val Lys Ser Lys Ser Ser Lys 145 150 155 160	80
gat aat cct tat cgc ggc tat tat ttc tgg aaa gat gct aaa gaa ggg 52 Asp Asn Pro Tyr Arg Gly Tyr Tyr Phe Trp Lys Asp Ala Lys Glu Gly 165 170 175	28

cag gcg cct aat aat tac cct tca ttc ttt ggt ggc tcg gcg tgg caa 576 Gln Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln aaa gat gaa aag acc aat caa tac tac ctg cac tat ttt gct aaa caa 624 Lys Asp Glu Lys Thr Asn Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln 195 cag cct gac cta aac tgg gat aat ccc aaa gtc cgt caa gat ctt tat 672 Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr 210 gca atg tta cgt ttc tgg tta gat aaa ggc gtg tct ggt tta cgt ttt 720 Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe 225 230 235 gat acg gta gcg acc tac tca aaa att ccg gat ttc cca aat ctc acc 768 Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asp Phe Pro Asn Leu Thr 245 caa caa cag ctg aag aat ttt gca gcg gag tat acc aag ggc cct aat 816 Gln Gln Gln Leu Lys Asn Phe Ala Ala Glu Tyr Thr Lys Gly Pro Asn 265 att cat cgt tac gtc aat gaa atg aat aaa gag gtc ttg tct cat tac 864 Ile His Arg Tyr Val Asn Glu Met Asn Lys Glu Val Leu Ser His Tyr 280 gac att gcg act gcc ggt gaa atc ttt ggc gta ccc ttg gat caa tcg 912 Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Gln Ser 295 300 ata aag ttc ttc gat cgc cgc cgt gat gag ctq aac att qca ttt acc 960 Ile Lys Phe Phe Asp Arg Arg Asp Glu Leu Asn Ile Ala Phe Thr 305 310 315 ttt gac tta atc aga ctc gat cga gac tct gat caa aga tgg cgt cga 1008 Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asp Gln Arg Trp Arg Arg aaa gat tgg aaa ttg tcg caa ttc cgg cag atc atc gat aac gtt gac 1056 Lys Asp Trp Lys Leu Ser Gln Phe Arg Gln Ile Ile Asp Asn Val Asp 340 cgt act gca gga gaa tat ggt tgg aat gcc ttc ttc ttg gat aac cac 1104 Arg Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His 355 gac aat ccg cgc gct gtc tcg cac ttt ggc gat gat gat cgc cca caa 1152 Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Asp Pro Gln 370 375 tgg cgt gag cca tcg gct aaa gcg ctt gca acc ttg acg ctg act caa 1200 Trp Arg Glu Pro Ser Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln 390 395 cga gca aca cct ttt att tat caa ggt tca gaa ttg ggc atg acc aat 1248 Arg Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn 410 tac ccg ttt aaa gct att gat gaa ttc gat gat att gag gtg aaa ggt 12.96 Tyr Pro Phe Lys Ala Ile Asp Glu Phe Asp Asp Ile Glu Val Lys Gly 425 ttt tgg cat gac tac gtt gag aca gga aag gtc aaa gcc gac gag ttc 1344 Phe Trp His Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Asp Glu Phe 435

										•						
										aac Asn						1392
										acg Thr 475						1440
										aat Asn						1488
										cgt Arg						1536
agg Arg	cat His	gac Asp 515	atc Ile	ccg Pro	gca Ala	ctg Leu	acc Thr 520	tat Tyr	ggt Gly	aca Thr	tac Tyr	acc Thr 525	gat Asp	ttg Leu	gat Asp	1584
cct Pro	gca Ala 530	aat Asn	gat Asp	tcg Ser	gtc Val	tac Tyr 535	gcc Ala	tat Tyr	aca Thr	cgc Arg	agc Ser 540	ctt Leu	ggg ggg	gcg Ala	gaa Glu	1632
										caa Gln 555						1680
										att Ile						1728
aaa Lys	aac Asn	gtg Val	gtg Val 580	aaa Lys	aag Lys	aat Asn	gat Asp	tca Ser 585	tta Leu	ctc Leu	gag Glu	cta Leu	aaa Lys 590	cca Pro	tgg Trp	1776
										aat Asn						1824
										ccg Pro		Phe				1872
		_	gca Ala		tag											1890
<212	.> 62 !> PF	P.				. 1										
		.ocaii	ILHOL	Jacte	er ru	ıbruı	n									
<400 Met 1		Arg	Gln	Gly 5	Leu	Lys	Thr	Ala	Leu 10	Ala	Ile	Phe	Leu	Thr 15	Thr	
Ser	Leu	Cys	Ile 20	Ser	Cys	Gln	Gln	Ala 25	Phe	Gly	Thr	Gln	Gln 30	Pro	Leu	
Leu	Asn	Glu 35	Lys	Ser	Ile	Glu	Gln 40	Ser	Lys	Thr	Ile	Pro 45	Lys	Trp	Trp	
Lys	Glu 50	Ala	Val	Phe	Tyr	Gln 55	Val	Tyr	Pro	Arg	Ser 60	Phe	Lys	Asp	Thr	
Asn 65	Gly	Asp	Gly	Ile	Gly 70	Asp	Ile	Asn	Gly	Ile 75	Ile	Glu	Lys	Leu.	Asp 80	

	Tyr	Leu	Lys	Ala	Leu 85	Gly	Ile	Asp	Ala	Ile 90	Trp	Ile	Asn	Pro	His 95	Tyr
	Asp	Ser	Pro	Asn 100	Thr	Asp	Asn	Gly	Tyr 105	Asp	Ile	Arg	Asp	Tyr 110	Arg	Lys
	Ile	Met	Lys 115		Tyr	Gly	Thr	Met 120	Glu	Asp	Phe	Asp	Arg 125	Leu	Ile	Ser
	Glu	Met 130	Lys	Lys	Arg	Asn	Met 135		Leu	Met	Ile	Asp 140	Val	Val	Ile	Asn
	His 145	Thr	Ser	Asp	Gln	Asn 150	Glu	Trp	Phe	Vạl	Lys 155	Ser	Lys	Ser	Ser	Lys 160
	Asp	Asn	Pro	Tyr	Arg 165	Gly	Tyr	Tyr	Phe	Trp 170	Lys	Asp	Ala	Ļys	Glu 175	Gly
	Gln	Ala	Pro	Asn 180	Asn	Tyr	Pro	Ser	Phe 185	Phe	Gly	Gly	Ser	Ala 190	Trp	Gln
	Lys	Asp	Glu 195	Lys	Thr	Asn	Gln	Tyr 200	Tyr	Leu	His	Tyr	Phe 205	Ala	Lys	Gln
•	Gln	Pro 210	Asp	Leu	Asn	Trp	Asp 215	Asn	Pro	Lys	Val	Arg 220	Gln	Asp	Leu	Tyr
	Ala 225	Met	Leu	Arg	Phe	Trp 230	Leu	Asp	Lys	Gly	Val 235	Ser	Gly	Leu	Arg	Phe 240
	Asp	Thr	Val	Ala	Thr 245	Tyr	Ser	Lys	Ile	Pro 250	Asp	Phe	Pro	Asn	Leu 255	Thr
	Gln	Gln	Gln	Leu 260	Lys	Asn	Phe	Ala	Ala 265	Glu	Tyr	Thr	Lys	Gly 270	Pro	Asn
	Ile	His	Arg 275	Tyr	Val	Asn	Glu	Met 280	Asn	Lys	Glu	Val	Leu 285	Ser	His	Tyr
	Asp	Ile 290	Ala	Thr	Ala	Gly	Glu 295	Ile	Phe	Gly	Val	Pro 300	Leu	Asp	Gln	Ser
	Ile 305	Lys	Phe	Phe	Asp	Arg 310	Arg	Arg	Asp	Glu	Leu 315	Asn	Ile	Ala	Phe	Thr 320
	Phe	Asp	Leu	Ile	Arg 325	Leu	Asp	Arg	Asp	Ser 330	Asp	Gln	Arg	Trp	Arg 335	Arg
	Lys	Asp	Trp	Lys 340	Leu	Ser	Gln	Phe	Arg 345	Gln	Ile	Ile	Asp	Asn 350	Val	Asp
	Arg	Thr	Ala 355	Gly	Glu	Tyr	Gly	Trp 360	Asn	Ala	Phe	Phe	Leu 365	Asp	Asn	His
	Asp	Asn 370	Pro	Arg	Ala	Val	Ser 375	His	Phe	Gly	Asp	Asp 380	Asp	Arg	Pro	Gln
	Trp 385	Arg	Glu	Pro	Ser	Ala 390	Lys	Ala	Leu	Ala	Thr 395	Leu	Thr	Leu	Thr	Gln 400
	Arg	Ala	Thr	Pro	Phe 405	Ile	Tyr	Gln	Gly	Ser 410	Glu	Leu	Gly	Met	Thr 415	Asn
	Tyr	Pro	Phe	Lys 420	Ala	Ile	Asp	Glu	Phe 425	Asp	Asp	Ile	Glu	Val 430	Lys	Gly
	Phe	Trp	His 435	Asp	Tyr	Val	Glu	Thr 440	Gly	Lys	Val	Lys	Ala 445	Asp	Glu	Phe
	Leu	Gln. 45.0.	Asn	Val	Arg	Leu	Thr 455	Ser	Arg	Asp	Asn	Ser 460	Arg	Thr	Pro	Phe

Gln Trp Asp Gly Ser Lys Asn Ala Gly Phe Thr Ser Gly Lys Pro Trp 475 Phe Lys Val Asn Pro Asn Tyr Gln Glu Ile Asn Ala Val Ser Gln Val Thr Gln Pro Asp Ser Val Phe Asn Tyr Tyr Arg Gln Leu Ile Lys Ile 505 Arg His Asp Ile Pro Ala Leu Thr Tyr Gly Thr Tyr Thr Asp Leu Asp 520 Pro Ala Asn Asp Ser Val Tyr Ala Tyr Thr Arg Ser Leu Gly Ala Glu Lys Tyr Leu Val Val Val Asn Phe Lys Glu Gln Met Met Arg Tyr Lys 550 555 Leu Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Asp Ser Asn Ser 570 Lys Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp 580 585 Gln Ser Gly Val Tyr Lys Thr Lys Ser Ile Asn Leu Ile Val Thr Pro Asn Asn Val Asn Ile Leu Lys Leu Leu Lys Pro Ala Phe Tyr Ala Gly 615 Phe Phe Ser Ala Lys 625 <210> 3 <211> 1305 <212> DNA -<213> Erwinia rhapontici <220> <221> CDS <222> (1)..(1305) <223> coding for N-terminal fragment of sucrose isomerase <400>. 3 atg tcc tct caa gga ttg aaa acg gct ntc gct att ttt ctt gca acc Met Ser Ser Gln Gly Leu Lys Thr Ala Xaa Ala Ile Phe Leu Ala Thr act ttt tct gcc aca tcc tat cag gcc tgc agt gcc nnn cca gat acc 96 Thr Phe Ser Ala Thr Ser Tyr Gln Ala Cys Ser Ala Xaa Pro Asp Thr 20 gcc ccc tca ctc acc gtt cag caa tca aat gcc ctg ccc aca tqq tqq Ala Pro Ser Leu Thr Val Gln Gln Ser Asn Ala Leu Pro Thr Trp Trp aag cag gct gtt ttt tat cag gta tat cca cgc tca ttt aaa gat acg 192 Lys Gln Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr 55 aat ggg gat ggc att ggg gat tta aac ggt att att gag aat tta gac Asn Gly Asp Gly Ile Gly Asp Leu Asn. Gly Ile Ile Glu Asn. Leu Asp 70 tat ctg aag aaa ctg ggt att gat gcg att tgg atc aat cca cat tac 288 Tyr Leu Lys Lys Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr

										7						
		ccg Pro														336
ata Ile	atg Met	aaa Lys 115	gaa Glu	tac Tyr	ggt Gly	acg Thr	atg Met 120	gaa Glu	gac Asp	ttt Phe	gac Asp	cgt Arg 125	ctt Leu	att Ile	tca Ser	384
		aag Lys														432
		agc Ser														480
		ccc Pro														528
		ccc Pro														576
		gat Asp 195														624
		gac Asp														672
		ctc Leu														720
		gtt Val														768
		cag Gln														816
		gac Asp 275														864
gat Asp	atc Ile 290	gcc Ala	act Thr	gcg Ala	Gly	gaa Glu 295	ata Ile	ttt Phe	ggg ggg	gtt Val	cct Pro 300	ctg Leu	gat Asp	aaa Lys	tcg Ser	912
att Ile 305	aag Lys	ttt Phe	ttc Phe	gat Asp	cgc Arg 310	cgt Arg	aga Arg	aat Asn	ga a Glu	tta Leu 315	Asn	ata Ile	gcg Ala	ttt Phe	acg Thr 32.0.	960
ttt Phe	gat Asp	ctg Leu	atc Ile	agg Arg 325	ctc Leu	gat Asp	cgt Arg	gat Asp	gct Ala 330	gat Asp	gaa Glu	aga Arg	tgg Trp	cgg Arg 335	cga Arg	1008
		tgg Trp														1056
		gca Ala 355														1104

										•							
gac Asp	aat Asn 370	ccc Pro	cgc Arg	gcg Ala	gtt Val	tct Ser 375	cac His	ttt Phe	ggt Gly	gat Asp	gat Asp 380	cga Arg	cca Pro	caa Gln	tgg Trp	1152	
cgc Arg 385	gag Glu	cat His	gcg Ala	gcg Ala	aaa Lys 390	gca Ala	ctg Leu	gca Ala	aca Thr	ttg Leu 395	acg Thr	ctg Leu	acc Thr	cag Gln	cgt Arg 400	1200	
gca Ala	acg Thr	ccg Pro	ttt Phe	atc Ile 405	tat Tyr	cag Gln	ggt Gly	Ser	gaa Glu 410	ctc Leu	ggt Gly	atg Met	acc Thr	aat Asn 415	tat Tyr	1248	
ccc Pro	ttt Phe	aaa Lys	aaa Lys 420	atc Ile	gat Asp	gat Asp	ttc Phe	gat Asp 425	gat Asp	gta Val	gag Glu	gtg Val	aaa Lys 430	ggt Gly	ttt Phe	1296	
	caa Gln	_		•								•				1305	
<211 <212	0> 4 L> 43 2> PI 3> E1	RT	ia rl	napoi	ntic	L							٠				
)> 4 Ser	Ser	Gln	Gly 5	Leu	Lys	Thr	Ala	Xaa 10	Ala	Ile	Phe	Leu	Ala 15	Thr		
Thr	Phe	Ser	Ala 20	Thr	Ser	Tyr	Gln	Ala 25	Cys	Ser	Ala	Xaa	Pro 30	Asp	Thr		
Ala	Pro	Ser-	Leu	Thr	Val	Gln	Gln 40	Ser	Asn	Ala	Leu	Pro 45	Thr	Trp	Trp		
Lys	Gln 50	Ala	Val	Phe	Tyr	Gln 55	Val	Tyr	Pro	Arg	Ser 60	Phe	Lys	Asp	Thr		
Asn 65	Gly	Asp	Gly	Ile	Gly 70	Asp	Leu	Asn	Gly	Ile 75	Ile	Glu	Asn	Leu	Asp 80		
Tyr	Leu	Lys	Lys	Leu 85	Gly	Ile	Asp	Ala	Ile 90	Trp	Ile	Asn	Pro	His 95	Tyr		
Asp	Ser	Pro	Asn 100	Thr	Asp	Asn	Gly	Tyr 105	Asp	Ile	Arg	Asp	Tyr 110	Arg	Lys		
Ile	Met	Lys 115	Glu	Tyr	Gly	Thr	Met 120	Glu	Asp	Phe	Asp	Arg 125	Leu	Ile	Ser		
Glu	Met 130	Lys	Lys	Arg	Asn	Met 135	Arg	Leu	Met	Ile	Asp 140	Ile	Val	Ile	Asn		
His 145	Thr	Ser	Asp	Gln	His 150	Ala	Trp	Phe	Val	Gln 155	Ser	Lys	Ser	Gly	Lys 160		
Asn	Asn	Pro	Tyr	Arg 165	Asp	Tyr	Tyr	Phe	Trp 170	Arg	Asp	Gly	Lys	Asp 175	Gly		
His	Ala	Pro	Asn 180	Asn	Tyr	Pro	Ser	Phe 185	Phe	Gly	Gly	Ser	Ala 190	Trp	Glu	•	
Lys	Asp	Asp 195	Lys	Ser	Gly	Gln	Tyr 200	Tyr	Leu	His	Tyr	Phe 205	Ala	Lys.	Gln		
Gln	Pro 21.0.	Asp	Leu	Asn	Trp	Asp 215	Asn	Pro	Lys	Val	Arg 220	Gln	Asp	Leu	Tyr	٠	
Asp 225	Met	Leu	Arg	Phe	Trp 230	Leu	Asp	Lys	Gly	Val 235	Ser	Gly	Leu	Arg	Phe 240	•	

Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asn Phe Pro Asp Leu Ser 250 Gln Gln Gln Leu Lys Asn Phe Ala Glu Glu Tyr Thr Lys Gly Pro Lys 265 Ile His Asp Tyr Val Asn Glu Met Asn Arg Glu Val Leu Ser His Tyr 2.80 Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Lys Ser Ile Lys Phe Phe Asp Arg Arg Asn Glu Leu Asn Ile Ala Phe Thr 310 315 Phe Asp Leu Ile Arg Leu Asp Arg Asp Ala Asp Glu Arg Trp Arg Arg 325 330 Lys Asp Trp Thr Leu Ser Gln Phe Arg Lys Ile Val Asp Lys Val Asp 340 345 Gln Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His 360 Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp 370 Arg Glu His Ala Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg 395 Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr 410 Pro Phe Lys Lys Ile Asp Asp Phe Asp Asp Val Glu Val Lys Gly Phe . 420 . 425 Trp Gln Asp 435 <210> 5 <211> 1803 <212> DNA <213> Erwinia rhapontici <220> <221> CDS <222> (1)..(1800) <223> coding for sucrose isomerase <400> 5 atg tcc tct caa gga ttg aaa acg gct gtc gct att ttt ctt gca acc Met Ser Ser Gln Gly Leu Lys Thr Ala Val Ala Ile Phe Leu Ala Thr act ttt tct gcc aca tcc tat cag gcc tgc agt gcc ggg cca gat acc Thr Phe Ser Ala Thr Ser Tyr Gln Ala Cys Ser Ala Gly Pro Asp Thr 25 gcc ccc tca ctc acc gtt cag caa tca aat gcc ctg ccc aca tgg tgg 144 Ala Pro Ser Leu Thr Val Gln Gln Ser Asn Ala Leu Pro Thr Trp 40 aag cag gct gtt ttt tat cag gta tat cca cgc tca ttt aaa gat acg Lys Gln Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr aat ggg gat ggc att ggg gat tta aac ggt att att gag aat tta gac Asn Gly Asp Gly Ile Gly Asp Leu Asn Gly Ile Ile Glu Asn Leu Asp

										9					
									att Ile 90						288
									gac Asp						336
									gac Asp						384
	-		-		_	_	_	_	atg Met		-	_			432
									gtt Val						480
									tgg Trp 170						528
•									ttc Phe						576
									ctc Leu						624
									aaa Lys						672
	-	_		_		 Leu	_		ggc Gly	_			_		720
	_		_	-		_			ccg Pro 250			_		_	768
									gaa Glu						816
									aga Arg						864
									ggg Gly						912
									gaa Glu				Phe		960
									gct Ala 330						1008
									aaa Lys					gac Asp,	1056

6	a a In	acg Thr	gca Ala 355	gga Gly	gag Glu	tat Tyr	gg g Gl y	tgg Trp 360	aat Asn	gcc Ala	ttt Phe	ttc Phe	tta Leu 365	gac Asp	aat Asn	cac His	1104
9 A	ac sp	aat Asn 370	ccc	cgc Arg	gcg Ala	gtt Val	tct Ser 375	cac His	ttt Phe	ggt Gly	gat Asp	gat Asp 380	cga Arg	cca Pro	caa Gln	tgg Trp	1152
A	gc rg 85	gag Glu	cat His	gcg. Ala	gcg Ala	aaa Lys 390	gca Ala	ctg Leu	gca Ala	aca Thr	ttg Leu 395	acg Thr	ctg Leu	acc Thr	cag Gln	cgt Arg 400	1200
9 A	ca la	acg Thr	ccg Pro	ttt Phe	atc Ile 405	tat Tyr	cag Gln	ggt Gly	tca Ser	gaa Glu 410	ctc Leu	ggt Gly	atg Met	acc Thr	aat Asn 415	tat Tyr	1248
P	ro	ttt Phe	aaa Lys	aaa Lys 420	atc	gat Asp	gat Asp	ttc Phe	gat Asp 425	gat Asp	gta Val	gag Glu	gtg Val	aaa Lys 430	ggt Gly	ttt Phe	1296
T	rp	Gln	Asp 435	Tyr	Val	Glu	Thr	Gly 440	Lys.	Val	Lys	gct Ala	Glu 445	Glu	Phe	Leu	1344
G	ln	Asn 450	Val	Arg	Gln	Thr	Ser 455	Arg	Asp	Asn	Ser	aga Arg 460	Thr	Pro	Phe	Gln	1392
T 4	rp 65	Asp	Ala	Ser	Lys	Asn 470	Ala	Gly	Phe	Thr	Ser 475		Thr	Pro	Ţrp	Leu 480	1440
L	ys	Ile	Asn	Pro	Asn 485	Tyr	Lys	Glu	Ile	Asn 490	Ser	gca Ala	Asp	Gln	Ile 495	Asn	1488
A	sn	Pro	Asn	Ser 500	Val	Phe	Asn	Tyr	Tyr 505	Arg	Lys	ctg Leu	Ile	Asn 510	Ile	Arg	1536
Н	is	Asp	Ile 515	Pro	Ala	Leu	Thr	Tyr 520	Gly	Ser	Tyr	att Ile	Asp 525	Leu	Asp	Pro	1584
A	sp	Asn 530	Asn	Ser	Val	Tyr	Ala 535	Tyr	Thr	Arg	Thr	ctc Leu 540	Gly	Ala	Glu	Lys	1632
T 5	yr 45	Leu	Val	Val	Ile	Asn 550	Phe	Lys	Glu	Glu	Val 555	atg Met	His	Tyr	Thr	Leu 560	1680
P	ro	Gly	Asp	Leu	Ser 565	Ile	Asn	Lys	Val	Ile 570	Thr	gaa Glu	Asn	Asn	Ser 575	His	1728
a T	ct hr	att Ile	gtg Val	aat. Asn 580	aaa Lys	aat Asn	gac Asp	agg Arg	caa Gln 585	ctc Leu	cgt Arg	ctt Leu	Glu	ccc Pro 590	tgg Trp	cag Gln	1776
				tat Tyr				ccg Pro 600	tag					٠			1803
		> 6 > 60	0														

<211> 600

<212> PRT

<213> Erwinia rhapontici

<400> 6 Met Ser Ser Gln Gly Leu Lys Thr Ala Val Ala Ile Phe Leu Ala Thr Thr Phe Ser Ala Thr Ser Tyr Gln Ala Cys Ser Ala Gly Pro Asp Thr 25 Ala Pro Ser Leu Thr Val Gln Gln Ser Asn Ala Leu Pro Thr Trp Trp 40 Lys Gln Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr Asn Gly Asp Gly Ile Gly Asp Leu Asn Gly Ile Ile Glu Asn Leu Asp Tyr Leu Lys Lys Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys 105 Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser 120 'Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Ile Val Ile Asn His Thr Ser Asp Gln His Ala Trp Phe Val Gln Ser Lys Ser Gly Lys 150 155 160 Asn Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Gly 165 His Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Glu 185 Lys Asp Asp Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln 200 Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr 215 Asp Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe 230 235 Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asn Phe Pro Asp Leu Ser 245 250 Gln Gln Gln Leu Lys Asn Phe Ala Glu Glu Tyr Thr Lys Gly Pro Lys 265 Ile His Asp Tyr Val Asn Glu Met Asn Arg Glu Val Leu Ser His Tyr 280 Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Lys Ser 295 300 Ile Lys Phe Phe Asp Arg Arg Asn Glu Leu Asn Ile Ala Phe Thr 305 310 315 Phe Asp Leu Ile Arg Leu Asp Arg Asp Ala Asp Glu Arg Trp Arg Arg 330 -Lys Asp Trp Thr Leu Ser Gln Phe Arg Lys Ile Val Asp Lys Val Asp 3.4.5 Gln Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His 360 Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp 3.80

Arg Glu His Ala Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg 390 395 Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr 405 410 Pro Phe Lys Lys Ile Asp Asp Phe Asp Asp Val Glu Val Lys Gly Phe 420 425 Trp Gln Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Glu Glu Phe Leu 440 Gln Asn Val Arg Gln Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln 455 Trp Asp Ala Ser Lys Asn Ala Gly Phe Thr Ser Gly Thr Pro Trp Leu 470 Lys Ile Asn Pro Asn Tyr Lys Glu Ile Asn Ser Ala Asp Gln Ile Asn 490 Asn Pro Asn Ser Val Phe Asn Tyr Tyr Arg Lys Leu Ile Asn Ile Arg 500 505 His Asp Ile Pro Ala Leu Thr Tyr Gly Ser Tyr Ile Asp Leu Asp Pro Asp Asn Asn Ser Val Tyr Ala Tyr Thr Arg Thr Leu Gly Ala Glu Lys 535 540 Tyr Leu Val Val Ile Asn Phe Lys Glu Glu Val Met His Tyr Thr Leu 550 555 Pro Gly Asp Leu Ser Ile Asn Lys Val Ile Thr Glu Asn Asn Ser His 565 570 Thr Ile Val Asn Lys Asn Asp Arg Gln Leu Arg Leu Glu Pro Trp Gln . 585 Ser Gly Ile Tyr Lys Leu Asn Pro 595 600 <210> 7 <211> 1803 <212> DNA <213> Protaminobacter rubrum <220> <221> CDS <222> (1)..(1800) <223> coding for sucrose isomerase <400> 7 atg ccc cgt caa gga ttg aaa act gca cta gcg att ttt cta acc aca 48 Met Pro Arg Gln Gly Leu Lys Thr Ala Leu Ala Ile Phe Leu Thr Thr tca tta tgc atc tca tgc cag caa gcc ttc ggt acg caa caa ccc ttg 96 Ser Leu Cys Ile Ser Cys Gln Gln Ala Phe Gly Thr Gln Gln Pro Leu 25 ctt aac gaa aag agt atc gaa cag tcg aaa acc ata cct aaa tgg tgg Leu Asn Glu Lys Ser Ile Glu Gln Ser Lys Thr Ile Pro Lys Trp Trp aag gag gct gtt ttt tat cag gtg tat ccg cgc tcc ttt aaa gac acc 1.9.2 Lys Glu Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr

							_						
				atc Ile									240
				ttg Leu 85									288
				acg Thr									336
				tat Tyr									384
				cgg Arg									432
				caa Gln									480
•				cgc Arg 165									528
				aat Asn									576
				acc Thr			_		•	_			624
				aac Asn									672
	-	_	_	ttc Phe		_					_		720
				acc Thr 245									768
				aag Lys									816
				gtc Val								tac Tyr	864
				gcc Ala				Val					912
				gat Asp									960
				aga Arg 325									1008

											. 4						
		_			-	_				_		atc Ile	_		-	-	1056
•	_		-		-					_		ttc Phe	_	_			1104
•						Val					Asp	gat Asp 380					1152
												acg Thr					1200
												ggc Gly					1248
												gag Glu					1296
												gcc Ala				ttg , Leu	1344
												cgg Arg 460					1392
												gga Gly					1440
												gta Val					1488
												ttg Leu					1536
												acc Thr					1584
												ctt Leu 540					1632
												atg Met					1680
	ccg Pro	gat Asp	aat Asn	tta Leu	tcc. Ser 565	att Ile	gag Glu	aaa Lys	gtg Val	att Ile 570	ata Ile	gac Asp	agc Ser	aac Asn	agc Ser 575	aaa Lys	1728
												cta Leu					1776
			gtt Val 595														1803

<210> 8 <211> 600 <212> PRT <213> Protaminobacter rubrum <400> 8 Met Pro Arg Gln Gly Leu Lys Thr Ala Leu Ala Ile Phe Leu Thr Thr Ser Leu Cys Ile Ser Cys Gln Gln Ala Phe Gly Thr Gln Gln Pro Leu 25 Leu Asn Glu Lys Ser Ile Glu Gln Ser Lys Thr Ile Pro Lys Trp Trp Lys Glu Ala Val Phe Tyr Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr Asn Gly Asp Gly Ile Gly Asp Ile Asn Gly Ile Ile Glu Lys Leu Asp Tyr Leu Lys Ala Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Arg Leu Ile Ser 120 Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn 135 His Thr Ser Asp Gln Asn Glu Trp Phe Val Lys Ser Lys Ser Ser Lys 150 155 Asp Asn Pro Tyr Arg Gly Tyr Tyr Phe Trp Lys Asp Ala Lys Glu Gly 170 Gln Ala Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln 180 Lys Asp Glu Lys Thr Asn Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln 200 Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Gln Asp Leu Tyr 215 Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Leu Arg Phe 230 Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Asp Phe Pro Asn Leu Thr 250 Gln Gln Gln Leu Lys Asn Phe Ala Ala Glu Tyr Thr Lys Gly Pro Asn 265 Ile His Arg Tyr Val Asn Glu Met Asn Lys Glu Val Leu Ser His Tyr 285 Asp Ile Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Gln Ser 295 Ile Lys Phe Phe Asp Arg Arg Asp Glu Leu Asn Ile Ala Phe Thr 315 Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asp GIn Arg Trp Arg Arg 330

Lys Asp Trp Lys Leu Ser Gln Phe Arg Gln Ile Ile Asp Asn Val Asp 340 345 350

Arg Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His 360 Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp 375 380 Arg Glu Pro Ser Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg 385 390 395 Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr 410 Pro Phe Lys Ala Ile Asp Glu Phe Asp Asp Ile Glu Val Lys Gly Phe 425 Trp His Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Asp Glu Phe Leu 440 Gln Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln 455 Trp Asp Gly Ser Lys Asn Ala Gly Phe Thr Ser Gly Lys Pro Trp Phe 470 475 Lys Val Asn Pro Asn Tyr Gln Glu IIe Asn Ala Val Ser Gln Val Thr 485 490 Gln Pro Asp Ser Val Phe Asn Tyr Tyr Arg Gln Leu Ile Lys Ile Arg 505 His Asp Ile Pro Ala Leu Thr Tyr Gly Thr Tyr Thr Asp Leu Asp Pro 520 Ala Asn Asp Ser Val Tyr Ala Tyr Thr Arg Ser Leu Gly Ala Glu Lys 535 Tyr Leu Val Val Val Asn Phe Lys Glu Gln Met Met Arg Tyr Lys Leu 555 Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Asp Ser Asn Ser Lys 570 Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp Gln 585 590 · Ser Gly Val Tyr Lys Leu Asn Gln <210> 9 <211> 1794 <212> DNA <213> Enterobacter sp. <220> <221> CDS <222> (1)...(1791) <223> coding for sucrose isomerase atg tot ttt gtt acg cta cgt acc ggg gtg gct gtc gcg ctg tca tct 48 Met Ser Phe Val Thr Leu Arg Thr Gly Val Ala Val Ala Leu Ser Ser . 10 ttg ata ata agt ctg gcc tgc ccg gct gtc agt gct gca cca tcc ttg 96 Leu Ile Ile Ser Leu Ala Cys Pro Ala Val Ser Ala Ala Pro Ser Leu aat cag gat att cac gtt caa aag gaa agt gaa tat cct gca tgg tgg Asn Gln Asp Ile His Val Gln Lys Glu Ser Glu Tyr Pro Ala Trp Trp

aaa Lys	gaa Glu 50	gct Ala	gtt Val	ttt Phe	tat Tyr	cag Gln 55	atc Ile	tat Tyr	cct Pro	cgc Arg	tca Ser 60	ttt Phe	aaa Lys	gac Asp	acc Thr	192
aat Asn 65	gat Asp	gat Asp	ggc Gly	att Ile	ggc Gly 70	gat Asp	att Ile	cgc Arg	ggt Gly	att Ile 75	Ile	gaa Glu	aag Lys	ctg Leu	gac Asp 80	240
tat Tyr	ctg Leu	aaa Lys	tcg Ser	ctc Leu 85	ggt Gly	att Ile	gac Asp	gct Ala	atc Ile 90	tgg Trp	atc Ile	aat Asn	ccc Pro	cat His 95	tac Tyr	288
Asp	Ser	Pro	Asn 100	Thr	gat Asp	Asn	Gly	Tyr 105	Asp	Ile	Ser	Asn	Tyr 110	Arg	Gln	336
Ile	Met	Lys 115	Glu	Tyr	ggc Gly	Thr	Met 120	Glu	Asp	Phe	Asp	Ser 125	Leu	Val	Ala	¸38 4
Glu	Met 130	Lys	Ĺys	Arg	aat Asn	Met 135	Arg	Leu	Met	Ile	Asp 140	Val	Val	Ile	Asn	432
cat His 145	acc Thr	agt Ser	gat Asp	caa Gln	cac His 150	ccg Pro	tgg Trp	ttt Phe	att Ile	cag Gln 155	agt Ser	aaa Lys	agc Ser	gat Asp	aaa Lys 160	480
Asn	Asn	Pro	Tyr	Arg 165	gac Asp	Tyr	Tyr	Phe	Trp 170	Arg	Asp	Gly	Lys	Asp 175	Asn	528
cag Gln	cca Pro	cct Pro	aat Asn 180	aat Asn	tac Tyr	ccc Pro	tca Ser	ttt Phe 185	ttc Phe	ggc Gly	ggc Gly	tcg Ser	gca Ala 190	tgg Trp	caa Gln	576
aaa Lys	gat Asp	gca Ala 195	aag Lys	tca Ser	gga Gly	cag Gln	tác Tyr 200	tat Tyr	tta Leu	cac His	tat Tyr	ttt Phe 205	gcc [°] Ala	aga Arg	cag Gln	624
Gln	Pro 210	Asp	Leu	Asn	tgg Trp	Asp 215	Asn	Pro	Lys	Val	Arg 220	Glu	Asp	Leu	Tyr	672
A1a 225	Met	Leu	Arg	Phe	tgg Trp 230	Leu	Asp	Lys	Gly	Val 235	Ser	Gly	Met	Arg	Phe 240	720
Asp	Thr	Val	Ala	Thr 245	tat Tyr	Ser	Lys	Ile	Pro 250	Gly	Phe	Pro	Asn	Leu 255	Thr	768
Pro	gaa Glu	caa Gln	cag Gln 260	aaa Lys	aat Asn.	ttt Phe	gct Ala	gaa Glu 265	caa Gln	tac Tyr	acc Thr	atg Met	ggd Xaa 270	cct Pro	aat Asn	816
att Ile	cat His	cga Arg 275	tac Tyr	att Ile	cag Gln	gaa Glu	atg Met 280	Asn	cgg Arg	aaa L <u>y</u> s	gtt Val	ctg Leu 285	tcc Ser	cgg Arg	tat Tyr	864
gat Asp	gtg Val 290	gcc Ala	acc [.] Thr	gcg Ala	ggt Gly	gaa Glu. 295	att Ile	ttt [.] Phe	ggc Gly	gtc Val	ccg Pro- 300	ctg Leu	gat. Asp _/	cgt. Arg	tcg Ser	912
tcg Ser 305	cag Gln	ttt Phe.	ttt Phe	gat Asp	cgc Arg 310:	cgc Arg	cga Arg	cat His	gag Glu	ctg Leu 315	aat Asn	atg Met	gcg [.] Ala.	ttt Phe	atg Met 320	960

						1	.8						
							aat Asn						1008
_	_	 _		-	_	_	atc Ile		_		_	_	1056
							ttc Phe						1104
_		_	 -				gat Asp	_		_			1152
							att Ile 395						1200
							ctg Leu						1248
	•			_	_	_	atc Ile		_				1296
							acg Thr						1344
							agc Ser						1392
							cgc Arg 475						1440
							scc Xaa						1488
							aaa Lys						1536
							tat Tyr						1584
							acg Thr						1632
							ccg Pro 555						1680
							att Ile						1728
							agc Ser						1:7:7:6 .

gcg tat aag ctg cgg taa Ala Tyr Lys Leu Arg 595 <210> 10 <211> 597 <212> PRT <213> Enterobacter sp. <400> 10 Met Ser Phe Val Thr Leu Arg Thr Gly Val Ala Val Ala Leu Ser Ser Leu Ile Ile Ser Leu Ala Cys Pro Ala Val Ser Ala Ala Pro Ser Leu 20 Asn Gln Asp Ile His Val Gln Lys Glu Ser Glu Tyr Pro Ala Trp Trp Lys Glu Ala Val Phe Tyr Gln Ile Tyr Pro Arg Ser Phe Lys Asp Thr Asn Asp Asp Gly Ile Gly Asp Ile Arg Gly Ile Ile Glu Lys Leu Asp 75 Tyr Leu Lys Ser Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Ser Asn Tyr Arg Gln Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Ser Leu Val Ala 120 Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn 135 140 His Thr Ser Asp Gln His Pro Trp Phe Ile Gln Ser Lys Ser Asp Lys 150 Asn Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Asn 165 170 Gln Pro Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln 185 Lys Asp Ala Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Arg Gln 200 Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Glu Asp Leu Tyr 215 220 Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Met Arg Phe 230 235 Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Gly Phe Pro Asn Leu Thr 250 Pro Glu Gln Gln Lys Asn Phe Ala Glu Gln Tyr Thr Met Xaa Pro Asn 260 270 Ile His Arg Tyr Ile Gln Glu Met Asn Arg Lys Val Leu Ser Arg Tyr 280 Asp Val Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Arg Ser 295 Ser Gln Phe Phe Asp Arg Arg His Glu Leu Asn Met Ala Phe Met 310 Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asn Glu Arg Trp Arg His

Lys Ser Trp Ser Leu Ser Gln Phe Arg Gln Ile Ile Ser Lys Met Asp 345 Val Thr Val Gly Lys Tyr Gly Trp Asn Thr Phe Phe Leu Asp Asn His 360 Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp Arg Glu Ala Ser Ala Lys Ala Leu Ala Thr Ile Thr Leu Thr Gln Arg 390 . 395 Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr 405 Pro Phe Arg Gln Leu Asn Glu Phe Asp Asp Ile Glu Val Lys Gly Phe 425 Trp Gln Asp Tyr Val Gln Ser Gly Lys Val Thr Ala Thr Glu Phe Leu 440 Asp Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln 455 Trp Asn Asp Thr Leu Asn Ala Gly Phe Thr Arg Gly Lys Pro Trp Phe 470 475 His Ile Asn Pro Asn Tyr Val Glu Ile Asn Xaa Glu Arg Glu Glu Thr 490 Arg Glu Asp Ser Val Leu Asn Tyr Tyr Lys Lys Met Ile Gln Leu Arg 505 His His Ile Pro Ala Leu Val Tyr Gly Ala Tyr Gln Asp Leu Asn Pro 515 520 Gln Asp Asn Thr Val Tyr Ala Tyr Thr Arg Thr Leu Gly Asn Glu Arg Tyr Leu Val Val Val Asn Phe Lys Glu Tyr Pro Val Arg Tyr Thr Leu 555 Pro Ala Asn Asp Ala Ile Glu Glu Val Val Ile Asp Thr Gln Gln 565 570 Gly Ala Pro His Ser Thr Ser Leu Ser Leu Ser Pro Trp Gln Ala Gly 580 585 Ala Tyr Lys Leu Arg 595 <210> 11 <211> 1803 <212> DNA <213> Serratia plymuthica <220> <221> CDS <222> (1)..(1800) <223> coding for sucrose isomerase atg ccc cgt caa gga ttg aaa act gca cta gcg att ttt cta acc aca. 48 Met Pro Arg Gln Gly Leu Lys Thr Ala Leu Ala Ile Phe Leu Thr Thr 10 tca tta age gte tca tge cag caa gee tta ggt acg caa caa eee ttg Ser Leu Ser Val Ser Cys Gln Gln Ala Leu Gly Thr Gln Gln Pro Leu 20.

							_	T .					
	_	_	-	_	-	_			ata Ile				144
									tcc Ser 60				192
									ata Ile				240
									atc Ile				288
									cgt Arg				336
									gac Asp				384
									gat Asp 140				432
									agt Ser				480
									gat Asp				528
									ggc Gly				576
									tat Tyr				624
									cgt Arg 220				672
									tct Ser			ttt Phe 240	720
									ttc Phe				768
									acc		Pro		816
									gtt Val				8 6,4°r
									ccc Pro 300				9:12:

									-							
	aaa Lys															960
	gac Asp															1008
	gag Glu															1056
	act Thr															1104
	aat Asn 370															1152
	gag Glu														cga Arg 400	1200
	acg Thr															1248
ccc Pro	ttc Phe	aaa Lys	gct Ala 420	att Ile	gat Asp	gaa Glu	ttc Phe	gat Asp 425	gat Asp	att Ile	gag Glu	gtg Val	aaa Lys 430	ggt Gly	ttt Phe	1296
	cat His															1344
caa Gln	aat Asn 450	gta Val	cgc Arg	ctg Leu	acg Thr	agc Ser 455	agg Arg	gat Asp	aac Asn	agc Ser	cgg Arg 460	aca Thr	ccg Pro	ttc Phe	caa Gln	1392
	gat Asp															1440
aag Lys	gtc Val	aat Asn	cca Pro	aac Asn 485	tac Tyr	cag Gln	gaa Glu	Ile	aat Asn 490	gcg Ala	gta Val	agt Ser	caa Gln	gtc Val 495	gca Ala	1488
	ccc Pro			Val												1536
cat His	aac Asn	atc Ile 515	ccg Pro	gca Ala	ctg Leu	acc Thr	tat Tyr 520	ggc Gly	aca Thr	tac Tyr	acc Thr	gat Asp 525	ttg Leu	gat Asp	cct Pro	1584
gca Ala	aat Asn 530	gat Asp	tcg Ser	gtc Val	tac Tyr	gcc Ala 535	tat Tyr	aca Thr	cgc Arg	agc Ser	ctt Leu 540	Gly	gcg Ala	gaa Glu	aaa Lys	1632
tat Tyr 545	ctt Leu	gtt Val	gtc Val	gtt Val	aac Asn 550	ttc Phe	cag Gln	ga a Glu	caa Glņ	gtg Val 555	atg Met	aga Arg	tat Tyr	aaa Lys	tta Leu 560	1680
	gat Asp															1728

aac	gtt Val	gto Val	aaa Lys 580	Lys	g aat S Asn	gat Asp	tcc Ser	tta Leu 585	Leu	gaa Glu	cta Leu	aaa Lys	cca Pro	Trp	cag Gln	1776
tca Ser	ggg Gly	gtt Val	tat Tyr	aaa	t cta Leu	aat Asn	caa Gln 600	taa					390			1803
<21 <21	.0> 1 .1> 6 .2> F .3>. S	OO RT	ıtia	plym	uthi	ca										
	0> 1 Pro		Gln	Gly	Leu	Lys	Thr	Ala	Leu	Ala	Ile	Phe	Leu	Thr	Thr	
1				5)				10				•	15		
			20					25					30			
Leu	Asn	35	Lys	Ser	Ile	Glu	Gln 40	Ser	Lys	Thr	Ile	Pro 45	Lys	Trp	Trp	
Lys	Glu 50	Ala	Val	Phe	Tyr	Gln 55	Val	Tyr	Pro	Arg	Ser 60	Phe	Lys	Asp	Thr	
Asn 65	Gly	Așp	Gly	Ile	Gly 70	Asp	Ile	Lys	Gly	Ile 75	Ile	Glu	Lys	Leu	Asp 80	
Tyr	Leu	Lys	Ala	Leu 85	Gly	Ile	Asp	Ala	Ile 90	Trp	Ile	Asn	Pro	His 95	Tyr	
Àsp	Ser	Pro	Asn 100	Thr	Asp	Asn	Gly	Tyr 105	Asp	Ile	Arg	Asp	Tyr 110		Lys	
Ile	Met	Lys 115	Glu	Tyr	Gly	Thr	Met 120	Glu	Asp	Phe	Asp	Arg 125	Leu	Ile	Ser	•
Glu	Met 130	Lys	Lys	Arg	Asn	Met 135	Arg	Leu	Met	Ile	Asp 140		Val	Ile	Asn	
His 145	Thr	Ser	Asp	Gln	Asn 150	Glu	Trp	Phe	Val	Lys 155	Ser	Lys	Ser	Ser	Lys 160	
Asp	Asn	Pro	Tyr	Arg 165	Gly	Tyr	Tyr	Phe	Trp 170	Lys	Asp	Ala	Lys	Glu 175	Gly	
Gln	Ala	Pro	Asn 180	Asn	Tyr	Pro	Ser	Phe 185	Phe	Gly	.Gly	Ser	Ala 190	Trp	Gln	
Lys	Asp	Glu 195	Lys	Thr	Asn	Gln	Tyr 200	Tyr	Leu	His	Tyr	Phe 205	Ala	Lys	Gl'n	
Gln	Pro 210	Asp	Leu	Asn	Trp	Asp 215	Asn	Pro	Lys	Val	Arg 220	Gln	Asp	Leu	Tyr	
Ala 225	Met	Leu	Arg	Phe	Trp 230	Leu	Asp	Lys	Gly	Val 235	Ser	Gly	Leu	Arg	Phe 240	
Asp	Thr	Val	Ala	Thr 245	Tyr	Ser	Lys	Ile	Pro 250	Asp	Phe	Pro	Asn	Leu 255		•
Gln	Gln	Gln	Leu 260	Lys	Asn	Phe	Ala	Ala 265	Glu	Tyr.	Thr	Lys	Gly 2.70		Asn	
Ile	His	Arg 275	Tyr	Val.	Asn	Glu.	Met 280	Ąsn	Arg	Glu	Val	Leu 285	Ser	His	Tyr	
Asp	Ile 290	Ala	Thr	Ala	Gly	Glu 2.95	Ile	Phe	Gly	Va:1	Pro 300	Leu	Asp	Gln	Ser	

Ile Lys Phe Phe Asp Arg Arg Arg Asp Glu Leu Asn Ile Ala Phe Thr Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asp Gln Arg Trp Arg Arg 325 . 330 Lys Glu Trp Lys Leu Ser Gln Phe Arg Gln Val Ile Asp Asn Val Asp 340 345 Arg Thr Ala Gly Glu Tyr Gly Trp Asn Ala Phe Phe Leu Asp Asn His 360 · Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp 370 375 Arg Glu Pro Ser Ala Lys Ala Leu Ala Thr Leu Thr Leu Thr Gln Arg 390 Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr Pro Phe Lys Ala Ile Asp Glu Phe Asp Asp Ile Glu Val Lys Gly Phe 420 425 Trp His Asp Tyr Val Glu Thr Gly Lys Val Lys Ala Asp Glu Phe Leu Gln Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln Trp Asp Thr Ser Lys Asn Ala Gly Phe Thr Ser Gly Lys Pro Trp Phe 475 Lys Val Asn Pro Asn Tyr Gln Glu Ile Asn Ala Val Ser Gln Val Ala 490 Gln Pro Asp Ser Val Phe Asn Tyr Tyr Arg Gln Leu Ile Lys Ile Arg 500 505 510 His Asn Ile Pro Ala Leu Thr Tyr Gly Thr Tyr Thr Asp Leu Asp Pro 520 525 Ala Asn Asp Ser Val Tyr Ala Tyr Thr Arg Ser Leu Gly Ala Glu Lys 535 Tyr Leu Val Val Val Asn Phe Gln Glu Gln Val Met Arg Tyr Lys Leu 550 555 Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Glu Ser Asn Ser Lys Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp Gln 585 Ser Gly Val Tyr Lys Leu Asn Gln

<210> 13

<211> 1844

<212> DNA

<213> Artificial sequence

<220>

<223> Description of the artificial sequence: coding for fusion protein of signal peptide from proteinase inhibitor I and sucrose isomerase from Erwinia rhapontici

<220>

<221> CDS

<222> (24)..(1835)

```
<220>
 <221> sig_peptide
 <222> (24)..(143)
 <223> signal peptide from proteinase inhibitor I
 <221> misc_feature
 <222> (144)..(1835)
 <223> coding for mature peptide of sucrose isomerase
       from Erwinia rhapontici
                                  (palI)
 <400> 13
 ggtaccctaa ttaattatcc atc atg gat gtt cac aag gaa gtt aat ttc gtt 53
                            Met Asp Val His Lys Glu Val Asn Phe Val
 gct 'tac cta cta att gtt ctt gga tta ttg gta ctt gta agc gcg atg
 Ala Tyr Leu Leu Ile Val Leu Gly Leu Leu Val Leu Val Ser Ala Met
 gag cat gtt gat gcg aag gct tgc acc gaa ttg ggg atc ctc acc gtt
                                                                     149
 Glu His Val Asp Ala Lys Ala Cys Thr Glu Leu Gly Ile Leu Thr Val
. cag caa tca aat gcc ctg ccc aca tgg tgg aag cag gct gtt ttt tat
                                                                     197
 Gln Gln Ser Asn Ala Leu Pro Thr Trp Trp Lys Gln Ala Val Phe Tyr
                               50
 cag gta tat cca cgc tca ttt aaa gat acg aat ggg gat ggc att ggg
                                                                     245
 Gln Val Tyr Pro Arg Ser Phe Lys Asp Thr Asn Gly Asp Gly Ile Gly
 gat tta aac ggt att att gag aat tta gac tat ctg aag aaa ctg ggt
                                                                     293
 Asp Leu Asn Gly Ile Ile Glu Asn Leu Asp Tyr Leu Lys Lys Leu Gly
                       80
 att gat gcg att tgg atc aat cca cat tac gat tcg ccg aat acg gat
                                                                     341
 Ile Asp Ala Ile Trp Ile Asn Pro His Tyr Asp Ser Pro Asn Thr Asp
                                      100
 aat ggt tat gac atc cgg gat tac cgt aag ata atg aaa gaa tac ggt
 Asn Gly Tyr Asp Ile Arg Asp Tyr Arg Lys Ile Met Lys Glu Tyr Gly
              110
 acg atg gaa gac ttt gac cgt ctt att tca gaa atg aag aaa cgc aat
                                                                     437
 Thr Met Glu Asp Phe Asp Arg Leu Ile Ser Glu Met Lys Lys Arg Asn
 atg cgt ttg atg att gat att gtt atc aac cac acc agc gat cag cat
                                                                     485
 Met Arg Leu Met Ile Asp Ile Val Ile Asn His Thr Ser Asp Gln His
                          145
 gcc tgg ttt gtt cag agc aaa tcg ggt aag aac aac ccc tac agg gac
                                                                     533
 Ala Trp Phe Val Gln Ser Lys Ser Gly Lys Asn Asn Pro Tyr Arg Asp
                                         . 165
 tat tac ttc tgg cgt gac ggt aag gat ggc cat gcc ccc aat aac tat
                                                                     581
 Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Gly His Ala Pro Asn Asn Tyr
 ccc tcc ttc ttc ggt ggc tca gcc tgg gaa aaa gac gat aaa tca ggc
                                                                     629
 Pro Ser Phe Phe Gly Gly Ser Ala Trp Glu Lys Asp Asp Lys Ser Gly
             190
                                  195
 cag tat tac ctc cat tac ttt gcc aaa cag caa ccc gac ctc aac tgg
                                                                     677
 Gln Tyr Tyr Leu His Tyr Phe Ala Lys Gln Gln Pro Asp Leu Asn Trp
         205
                              210
```

								•					
											cgc Arg		725 .
	_		_			_		_		_	gcc Ala		773
_		_			_		_		_	_	tta Leu		821
											tac Tyr 280		869
											act Thr		917
											ttc Phe		965
_	_	-			-		•		_	_	atc Ile		1013
											acc Thr		1061
											gga Gly 360		1109
											cgc Arg		1157
											gcg Ala		1205
											ttt Phe		1253
											aaa Lys		1301
											tac Tyr 440		1349
											cgc Arg		1397
					Pro						agc Ser		1445
											ccc ⁻ Pro		1493

aaa Lys	gaa Glu	atc Ile	aac Asn	agc Ser 495	gca Ala	gat Asp	cag Gln	att Ile	aat Asn 500	aat Asn	cca Pro	aat Asn	tcc Ser	gta Val 505	ttt Phe	1541
aac Asn	tat Tyr	tat Tyr	aga Arg 510	aag Lys	ctg Leu	att 'Ile	aac Asn	att Ile 515	cgc Arg	cat His	gac Asp	atc Ile	cct Pro 520	gcc Ala	ttg Leu	1589
acc Thr	tac Tyr	ggc Gly 525	agt Ser	tat Tyr	att Ile	Asp	tta Leu 530	gac Asp	cct Pro	gac Asp	aac Asn	aat Asn 535	tca Ser	gtc Val	tat Tyr	1637
gct Ala	tac Tyr 540	acc Thr	cga Arg	acg Thr	ctc Leu	ggc Gly 545	gct Ala	gaa Glu	aaa Lys	tat Tyr	ctt Leu 550	gtg Val	gtc Val	att Ile	aat Asn	1685
ttt Phe 555	aaa Lys	gaa Glu	gaa Glu	gtg Val	atg Met 560	cac His	tac Tyr	acc Thr	ctg Leu	ccc Pro 565	Gly	gat Asp	tta Leu	tcc Ser	atc Ile 570	1733
aat Asn	aag Lys	gtg Val	att Ile	act Thr 575	gaa Glu	aac Asn	aac Asn	agt Ser	cac His 580	áct Thr	att Ile	gtg Val	aat Asn	aaa Lys 585	aat Asn	1781
Asp	agg Arg	Gln	Leu 590	Arg	ctt Leu	gaa Glu	ccc Pro	tgg Trp 595	cag Gln	tcg Ser	ggc Gly	att Ile	tat Tyr 600	aaa Lys	ctt Leu	1829
	ccg Pro	tag	gtcga	ac											•	1844
	0> 14	1 .														
							•							•	•	
<211> 604 <212> PRT <213> Artificial sequence															•	
<21:	3> A1	ctif:	icia.	L sec	quenc	e e									•	•
	3> De	escr	iptio	on o	E the	art	cific	cial	sequ	ience	e: co	oding	g for	r		
	3> D∈ fu ir	escr: usion nhib:	iption pro itor	on o: otein I an		art sigr	nal p	pepti	ide i	Erom	prot	teina	ase	r	•	·
<223	3> De fu ir rh	scri sion hib: napon	iption	on o: otein I an	then of	art sigr	nal p	pepti	ide i	Erom	prot	teina	ase	r	·	
<400	3> De fu ir rh 0> 14	escri usion hib: napon	iption pro itor ntici	on o oteir I ar L	then of	e art sign cros	nal p se is	pepti some:	ide i	from from	prot	teina vinia	ase a		Val	
<223	3> De fi ir rh O> 14 Asp	escri sion hibi napon Val	iption proitor itor itic:	on on I and Lys 5	then of nd su	e art sign cros	nal p se is Asn	epti some: Phe	val	from fron Ala	prot n Erv Tyr	teina vinia Leu	ase a Leu	Ile 15	`	
<223	3> De fu ir rh 0> 14	escri sion hibi napon Val	iption proitor itor itic:	on on I and Lys 5	then of nd su	e art sign cros	nal p se is Asn	epti some: Phe	Val 10 Met	from fron Ala	prot n Erv Tyr	teina vinia Leu	ase a Leu	Ile 15 Ala	`	
<400 Met 1 Leu	3> Definition of the first section of the first sec	escrision hibinapon Val Leu Thr	iption production production His Leu 20 Glu	on or otein I an i Lys 5 Val	f then of nd su Glu Leu Gly	e art sign cros Val Val	Asn Ser Leu 40	Phe Ala 25	Val 10 Met	from from Ala Glu Gln	prot n Erv Tyr His	Leu Val Ser 45	Leu Asp 30 Asn	Ile 15 Ala Ala	Lys Leu	
<400 Met 1 Leu	3> Definition of the first file of the fil	escrision hibinapon Val Leu Thr	iption production production His Leu 20 Glu	on or otein I an i Lys 5 Val	f then of nd su Glu Leu Gly	e art sign cros Val Val	Asn Ser Leu 40	Phe Ala 25	Val 10 Met	from from Ala Glu Gln	prot n Erv Tyr His	Leu Val Ser 45	Leu Asp 30 Asn	Ile 15 Ala Ala	Lys Leu	
<400 Met 1 Leu Ala Pro	3> Definition of the second se	escrision hibs hapon Val Leu Thr 35 Trp Asp	iptic n pro itor ntic: His Leu 20 Glu Trp	Lys Val Lys Asn	Glu Leu Gly Gln Gly 70	val Val Ile Ala 55 Asp	Asn Ser Leu 40 Val	Phe Ala 25 Thr Phe	Val 10 Met Val Tyr	from from Ala Glu Gln Asp 75	Tyr His Gln Val 60 Leu	Leu Val Ser 45 Tyr Asn	Leu Asp 30 Asn Pro	Ile 15 Ala Ala Arg	Lys Leu Ser Ile 80	
<400 Met 1 Leu Ala Pro	3> Definition of the first section of the first sec	escrision hibs hapon Val Leu Thr 35 Trp Asp	iptic n pro itor ntic: His Leu 20 Glu Trp	Lys Val Lys Asn	Glu Leu Gly Gln Gly 70	val Val Ile Ala 55 Asp	Asn Ser Leu 40 Val	Phe Ala 25 Thr Phe	Val 10 Met Val Tyr	from from Ala Glu Gln Asp 75	Tyr His Gln Val 60 Leu	Leu Val Ser 45 Tyr Asn	Leu Asp 30 Asn Pro	Ile 15 Ala Ala Arg	Lys Leu Ser Ile 80	
<400 Met 1 Leu Ala Pro Phe 65 Glu Asn	3> Definition of the second se	escrision hibs hapon Val Leu Thr 35 Trp Asp Leu His	ipticing production production. His Leu 20 Glu Trp Thr Asp Tyr 100	Lys Val Lys Asn Tyr 85	Glu Gly Gly 70 Leu Ser	val Val Ala 55 Asp Lys	Asn Ser Leu 40 Val Gly Lys Asn	Phe Ala 25 Thr Phe Ile Leu Thr 105	Val 10 Met Val Tyr Gly Gly 90 Asp	From from from Ala Glu Gln Asp 75 Ile Asn	Tyr His Gln Val 60 Leu Asp	Leu Val Ser 45 Tyr Asn Ala	Leu Asp 30 Asn Pro Gly Ile Asp 110	Ile 15 Ala Ala Arg Ile Trp 95	Lys Leu Ser Ile 80 Ile Arg	
<400 Met 1 Leu Ala Pro Phe 65 Glu Asn	3> Definition of the first state	escrision hibs hapon Val Leu Thr 35 Trp Asp Leu His	ipticing production production. His Leu 20 Glu Trp Thr Asp Tyr 100	Lys Val Lys Asn Tyr 85	Glu Gly Gly 70 Leu Ser	val Val Ala 55 Asp Lys	Asn Ser Leu 40 Val Gly Lys Asn	Phe Ala 25 Thr Phe Ile Leu Thr 105	Val 10 Met Val Tyr Gly Gly 90 Asp	From from from Ala Glu Gln Asp 75 Ile Asn	Tyr His Gln Val 60 Leu Asp	Leu Val Ser 45 Tyr Asn Ala	Leu Asp 30 Asn Pro Gly Ile Asp 110	Ile 15 Ala Ala Arg Ile Trp 95	Lys Leu Ser Ile 80 Ile Arg	
<400 Met 1 Leu Ala Pro Phe 65 Glu Asn Asp	3> Definition of the second se	val Leu Thr 35 Trp Asp Leu His Arg 115 Ile	ipticing production production production. His Leu 20 Glu Trp Thr Asp Tyr 100 Lys Ser	Lys Val Leu Lys Asn Tyr 85 Asp Ile Glu	Glu Leu Gly Gln Cly 70 Leu Ser Met	val Val Ala 55 Asp Lys Pro Lys Lys 135	Asn Ser Leu 40 Val Gly Lys Asn Glu 120 Lys	Phe Ala 25 Thr Phe Ile Leu Thr 105 Tyr Arg	Val 10 Met Val Tyr Gly 90 Asp Gly Asn	From from from Ala Glu Gln Gln 75 Ile Asn Thr	Tyr His Gln Val 60 Leu Asp Gly Met Arg	Leu Val Ser 45 Tyr Asn Ala Tyr Glu: 125 Leu.	Leu Asp 30 Asn Pro Gly Ile Asp 110 Asp Met	Ile 15 Ala Ala Arg Ile Trp 95 Ile Phe	Lys Leu Ser Ile 80 Ile Arg Asp	

										•						
	Lys	Ser	Gly	Lys	Asn 165	Asn	Pro	Tyr	Arg	Asp 170	Tyr	Tyr	Phe	Trp	Arg 175	Asp
	Gly	Lys	Asp	Gly 180	His	Ala	Pro	Asn	Asn 185	Tyr	Pro	Ser	Phe	Phe 190	Gly	Gly
	Ser	Ala	Trp 195	Glu	Lys	Asp	Asp	Lys 200	Ser	Gly	Gln	Tyr	Tyr 205	Leu	His	Tyr
	Phe	Ala 210	Lys	Gln	Gln	Pro	Asp 215	Leu	Asn	Trp	Asp	Asn 220	Pro	Lys	Val	Arg
	Gln 225	Asp	Leu	Tyr	Asp	Met 230	Leu	Arg	Phe	Trp	Leu 235	Asp	Lys	Gly	Val	Ser 240
	Gly	Leu	Arg	Phe	Asp 245	Thr	Val	Ala	Thr	Tyr 250	Ser	Lys	Ile	Pro	Asn 255	Phe
	Pro	Asp	Leu	Ser 260	Gln	Gln	Gln	Leu	Lys 265	Asn	Phe	Ala	Glu	Glu 270	Tyr	Thr
	Lyş	Gly	Pro 275	Lys	Ile	His	Asp	Tyr 280	Val	Asn	Glu	Met	Asn 285	Arg	Glu	Val
	<u>L</u> eu	Ser 290	His	Tyr	Asp	Ile	Ala 295	Thr	Ala	Gly	Glu	Ile 300	Phe	Gly	Val	Pro
	Leu 305	Asp	Lys	Ser	Ile	Lys 310	Phe	Phe	Asp	Arg	Arg 315	Arg	Asn	Glu	Leu	Asn 320
	Ile	Ala	Phe	Thr	Phe 325	Asp	Leu	Ile	Arg	Leu 330	Asp	Arg	Asp	Ala	Asp 335	Gļu
	Arg	Trp	Arg	Arg 340	Lys	Asp	Trp	Thr	Leu 345	Ser	Gln	Phe	Arg	Lys 350	Ile	Val
	Asp	Lys	Val 355	Asp	Gln	Thr	Ala	Gly 360	Glu	Tyr	Gly	Trp	Asn 365	Ala	Phe	Phe
	Leu	Asp 370	Asn	His	Asp	Asn	Pro 375	Arġ	Ala	Val	Ser	His 380	Phe	Gly	Asp	Asp
	Arg 385	Pro	Gln	Trp	Arg	Glu 390	His	Ala	Ala	Lys	Ala 395	Leu	Ala	Thr	Leu	Thr 400
	Leu	Thr	Gln	Arg	Ala 405	Thr	Pro	Phe	Ile	Tyr 410	Gln	Gly	Ser	Glu ⁻	Leu 415	Gly
	Met	Thr	Asn	Tyr 420	Pro	Phe	Lys	Lys	Ile 425	Asp	Asp	Phe	Asp	Asp 430	Val	Glu
	Val	Lys	Gly 435	Phe	Trp	Gln	Asp	Tyr 440	Val	Glu	Thr	Gly	Lys 445	Val	Lys	Ala
	Glu	Glu 450	Phe	Leu	Gln	Asn	Val 455	Arg	Gln	Thr	Ser	Arg 460	Asp	Asn	Ser	Arg
	Thr 465	Pro	Phe	Gln	Trp	Asp 470	Ala	Ser	Lys	Asn	Ala 475	Gly	Phe	Thr	Ser	Gly 480
	Thr	Pro	Trp	Leu	Lys 485	Ile	Asn	Pro	Asn	Tyr 490	Lys	Glu	Ile	Asn	Ser 495	Ala
•	Asp	Gln	Ile	Asn 500	Asn	Pro	Asn	Ser	Val 505	Phe	Asn	Tyr	Tyr	Arg 510	Lys	Leu
	Ile	Asn	Ile 515	Arg	His	Asp	Ile	Pro 520	Ala	Leu	Thr	Tyr	Gly 525	Ser	Tyr .	Ile
	Asp	Leu 530	Asp	Pro	Asp	Asn	Asn 535	Ser	Val	Tyr	Ala	Tyr 540	Thr	Arg	Thr	Leu

Gly Ala Glu Lys Tyr Leu Val Val Ile Asn Phe Lys Glu Glu Val Met

His Tyr Thr Leu Pro Gly Asp Leu Ser Ile Asn Lys Val Ile Thr Glu Asn Asn Ser His Thr Ile Val Asn Lys Asn Asp Arg Gln Leu Arg Leu 580 585 Glu Pro Trp Gln Ser Gly Ile Tyr Lys Leu Asn Pro 600 <210> 15 <211> 2477. <212> DNA <213> Klebsiella sp. <220> <221> CDS <222> (214)..(2007) <223> coding for sucrose isomerase gatatcactg gtattatgga gtattatact cccccttat ttactcatca aagccaggcg 60 ttccactctg cctccggtat ataactttcc gggaaacaat cccttcctga aaataattat 120 tgttaccgga gtcatactct ggctattgat gatttacgct tttctttaat aacaattcgt 180 ctcattcaca actgactttg caaggaaatt att atg tct ttt gtt acg cta cgt Met Ser Phe Val Thr Leu Arg acc ggg gtg gct gtc gcg ctg tca tct ttg ata ata agt ctg gcc tgc 282 . Thr Gly Val Ala Val Ala Leu Ser Ser Leu Ile Ile Ser Leu Ala Cys ccg gct gtc agt gct gca cca tcc ttg aat cag gat att cac gtt caa 330 Pro Ala Val Ser Ala Ala Pro Ser Leu Asn Gln Asp Ile His Val Gln 25 30 aag gaa agt gaa tat cct gca tgg tgg aaa gaa gct gtt ttt tat cag 378 Lys Glu Ser Glu Tyr Pro Ala Trp Trp Lys Glu Ala Val Phe Tyr Gln 40 45 atc tat cct cgc tca ttt aaa gac acc aat gat gat ggc att ggc gat 426 Ile Tyr Pro Arg Ser Phe Lys Asp Thr Asn Asp Asp Gly Ile Gly Asp 70. att cgc ggt att att gaa aag ctg gac tat ctg aaa tcg ctc ggt att 474 Ile Arg Gly Ile Ile Glu Lys Leu Asp Tyr Leu Lys Ser Leu Gly Ile 75 80 gac gct atc tgg atc aat ccc cat tac gac tct ccg aac acc gat aac 522 Asp Ala Ile Trp Ile Asn Pro His Tyr Asp Ser Pro Asn Thr Asp Asn ggc tat gac atc agt aat tat cgt cag ata atg aaa gag tat ggc aca 570 Gly Tyr Asp Ile Ser Asn Tyr Arg Gln Ile Met Lys Glu Tyr Gly Thr 105 110 atg gag gat ttt gat agc ctt gtt gcc gaa atg aaa aaa cga aat atg 618 Met Glu Asp Phe Asp Ser Leu Val Ala Glu Met Lys Lys Arg Asn Met 120 125 130 cgc tta atg atc gac gtg gtc att acc agt gat caa cac ccg 666 Arg Leu Met Ile Asp Val Val Ile Asn His Thr Ser Asp Gln His Pro 140

										30						
tgg	ttt Phe	att lle	caç Glr 155	ı Ser	aaa Lys	ago Ser	gat Asp	aaa Lys 160	Asn	aac Asn	cct Pro	tat Tyr	cgt Arg 165	Asp	tat Tyr	714
tat Tyr	tto Phe	tgg Trp	Arc	gac J Asp	gga Gly	aaa Lys	gat Asp 175	Asn	cag Glr	g cca Pro	cct Pro	aat Asn 180	Asn	tac Tyr	ccc	762
tca Ser	ttt Phe 185	: Pn∈	ggc Gly	ggc Gly	tcg Ser	gca Ala 190	Trp	caa Gln	aaa Lys	gat Asp	gca Ala	Lys	tca Ser	gga Gly	cag Gln	810
200	туг	Leu	HIS	Tyr	205	Ala	. Arg	Gln	Gln	210	Asp	Leu	Asn	Trp	gat Asp 215	858
ASN	PIO	· rAz	val	220	Glu	Asp	Leu	Tyr	Ala 225	Met	Leu	Arg	Phe	Trp 230		906
Asp	rås	GIY	235	Ser	Gly	Met	Arg	Phe 240	Asp	Thr	Val	Ala	Thr 245	Tyr	tcc Ser	954
rys	TTE	250	GIĀ	Phe	ccc Pro	Asn	Leu 255	Thr	Pro	_, Glu	Gln	Gln 260	Lys	Asn	Phe	1002
Ϋ́Та	265	Gin	Tyr	Thr	atg Met	Gly 270	Pro	Asn	Ile	His	Arg 275	Tyr	Ile	Gln	Glu	.1050
280	Asn	Arg	rys	Val	ctg Leu 285	Ser	Arg	Tyr	Asp	Val 290	Ala	Thr	Ala	Gly	Glu 295	1098
116	Pne	СТĀ	val	300	ctg Leu	Asp	Arg	Ser	Ser 305	Gln	Phe	Phe	Asp	Arg 310	Arg	1146
Arg	HIS	GIU	115 315	Asn	atg Met	Ala	Phe	Met 320	Phe	Asp	Leu	Ile	Arg 325	Leu	Asp	1194
Arg	ASP	330	Asn	GIu	cgc Arg	Trp	Arg 335	His	Lys	Ser	Trp	Ser 340	Leu	Ser	Gln	1242
Pne	345	GIN	iie	ile	agc Ser	Lys 350	Met	Asp	Val	Thr	Val 355	Gly	Lys	Tyr	Gly	1290
360	ASN	Thr	Pne	Pne	tta Leu 365	Asp	Asn	His	Asp	Asn 37.0	Pro	Arg	Ala	Val.	Ser 375	1338
птъ	rne	GTĀ	Asp	380	agg Arg	Pro	Gln.	Trp.	Arg 385	Glu	Ala	Ser	Ala	Lys 390	Ala	1386
Leu	Ата	Tnr	395	Thr	ctc Leu	Thr	GIn.	Arg 400	Ala	Thr	Pro	Phe	Ile 405	Tyr	Gln	14:34
ggt Gly	tca Ser	gag Glu 410	ctg Leu	gga Gly	atg Met	Thr	aat Asn. 415	tat Tyr	ccc Pro	ttc: Phe	agg [.] Arg	caa Gln 420	ctc Leu	aac: Asn.	gaa Gľu	1482

Phe Asp As 425	ac atc gag gto sp Ile Glu Vai	Lys Gly Phe 430	Trp Gln As	sp Tyr Val 35	Gln Ser
Gly Lys Va 440	cc acg gcc aca al Thr Ala Thi 44!	Glu Phe Leu	Asp Asn Va 450	al Arg Leu	Thr Ser 455
Arg Asp As	ac agc aga aca sn Ser Arg Thi 460	Pro Phe Gln	Trp Asn As	sp Thr Leu	Asn Ala 470
ggt ttt ac Gly Phe Th	et cgc gga aad or Arg Gly Lys 475	g ccg tgg ttt s Pro Trp Phe 480	cac atc aa His Ile As	ac cca aac sn Pro Asn 485	tat gtg 1674 Tyr Val
gag atc aa Glu Ile As 49	ac gcc gaa cgo sn Ala Glu Aro 90	gaa gaa acc Glu Glu Thr 495	cgc gaa ga Arg Glu As	at tca gtg sp Ser Val 500	ctg aat 1722 Leu Asn
tac tat aa Tyr Tyr Ly 505	aa aaa atg ati vs Lys Met Ile	cag cta cgc Gln Leu Arg 510	cac cat at His His Il 51	e Pro Ala	ctg gta 1770 Leu Val
tat ggc gc Tyr Gly Al 520	cc tat cag gat La Tyr Gln Asp 525	Leu Asn Pro	cag gac aa Gln Asp As 530	at acc gtt on Thr Val	tat gcc 1818 Tyr Ala 535
Tyr Thr Ar	ga acg ctg ggt cg Thr Leu Gly 540	Asn Glu Arg	Tyr Leu Va 545	al Val Val	Asn Phe 550
Lys Glu Ty	c ccg gtc cgc r Pro Val Arc 555	Tyr Thr Leu 560	Pro Ala As	n Asp Ala 565	Ile Glu
Glu Val Va 57		Gln Gln Gln 575	Ala Ala Al	a Pro His 580	Ser Thr
tcc ctg tc Ser Leu Se 585	a ttg agc cco r Leu Ser Pro	tgg cag gca Trp Gln Ala 590	ggt gtg ta Gly Val Ty 59	r Lys Leu	cgg 2007 Arg
	•	•			gtctttagc 2067
				and the second s	tctcatggc 2127
					agttagcat 2187
cccctgaaa	. gatggggg t a	tgtataaat ta	gcgttaaa ga	acatgaac c	agccaccgt 2247
					tgccgttga 2307
tgcgcctgaa	gcctcgccct t	tagggcc <mark>gg</mark> gaa	aataagca ca	gcatctgg c	gatctcttt 2367
					catcaggag 2427
	ggtcgtgtat a	tgagccagg cca	aaaaaag gt	gtgatatc	2477
<210> 16 <211> 598 <212> PRT <213> Kleb	, siella sp.				
<400> 16					
Met Ser Pho	e Val Thr Leu 5	Arg Thr Gly	Val Ala Va.	l Ala Leu :	Ser Ser 15 [.]
Leu Ile Ile	e Ser Leu Ala 20	Cys Pro Ala 25	Val Ser Al	a Ala Pro : 30	

Asn Gln Asp Ile His Val Gln Lys Glu Ser Glu Tyr Pro Ala Trp Trp Lys Glu Ala Val Phe Tyr Gln Ile Tyr Pro Arg Ser Phe Lys Asp Thr Asn Asp Asp Gly Ile Gly Asp Ile Arg Gly Ile Ile Glu Lys Leu Asp Tyr Leu Lys Ser Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Ser Asn Tyr Arg Gln 100 Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Ser Leu Val Ala 120 Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn His Thr Ser Asp Gln His Pro Trp Phe Ile Gln Ser Lys Ser Asp Lys 150 Asn Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Asn 170 Gln Pro Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln 185 Lys Asp Ala Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Arg Gln Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Glu Asp Leu Tyr Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Met Arg Phe 230 235 Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Gly Phe Pro Asn Leu Thr 245 Pro Glu Gln Gln Lys Asn. Phe Ala Glu Gln Tyr Thr Met Gly Pro Asn 265 Ile His Arg Tyr Ile Gln Glu Met Asn Arg Lys Val Leu Ser Arg Tyr 280 Asp Val Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Arg Ser 290 Ser Gln Phe Phe Asp Arg Arg His Glu Leu Asn Met Ala Phe Met 310 315 Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asn Glu Arg Trp Arg His 330 Lys Ser Trp Ser Leu Ser Gln Phe Arg Gln Ile Ile Ser Lys Met Asp 345 Val Thr Val Gly Lys Tyr Gly Trp Asn Thr Phe Phe Leu Asp Asn His 355 360 Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp 375 Arg Glu Ala Ser Ala Lys Ala Leu Ala Thr Ile Thr Leu Thr Gln Arg 395 Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr 410

Pro Phe Arg Gln Leu Asn Glu Phe Asp Asp Ile Glu Val Lys Gly Phe 420 425 Trp Gln Asp Tyr Val Gln Ser Gly Lys Val Thr Ala Thr Glu Phe Leu 440 Asp Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln 455 Trp Asn Asp Thr Leu Asn Ala Gly Phe Thr Arg Gly Lys Pro Trp Phe 470 475 . His Ile Asn Pro Asn Tyr Val Glu Ile Asn Ala Glu Arg Glu Glu Thr 485 490 Arg Glu Asp Ser Val Leu Asn Tyr Tyr Lys Lys Met Ile Gln Leu Arg 500 505 His His Ile Pro Ala Leu Val Tyr Gly Ala Tyr Gln Asp Leu Asn Pro 520 Gln Asp Asn Thr Val Tyr Ala Tyr Thr Arg Thr Leu Gly Asn Glu Arg , 530 535 Tyr Leu Val Val Val Asn Phe Lys Glu Tyr Pro Val Arg Tyr Thr Leu 550 555 Pro Ala Asn Asp Ala Ile Glu Glu Val Val Ile Asp Thr Gln Gln 570 Ala Ala Pro His Ser Thr Ser Leu Ser Leu Ser Pro Trp Gln Ala 585 Gly Val Tyr Lys Leu Arg 595 <210> 17 <211> 1797 <212> DNA <213> Klebsiella sp. <220> <221> CDS <222> (1)..(1794) <223> coding for sucrose isomerase atg tot tit git acg cta cgt acc ggg gtg gct gtc gcg ctg tca tot 48 Met Ser Phe Val Thr Leu Arg Thr Gly Val Ala Val Ala Leu Ser Ser ttg ata ata agt ctg gcc tgc ccg gct gtc agt gct gca cca tcc ttg Leu Ile Ile Ser Leu Ala Cys Pro Ala Val Ser Ala Ala Pro Ser Leu 20 aat cag gat att cac gtt caa aag gaa agt gaa tat cct gca tgg tgg Asn Gln Asp Ile His Val Gln Lys Glu Ser Glu Tyr Pro Ala Trp Trp aaa gaa gct gtt ttt tat cag atc tat cct cgc tca ttt aaa gac acc 192. Lys Glu Ala Val Phe Tyr Gln Ile Tyr Pro Arg Ser Phe Lys Asp Thr 55 aat gat gat ggc att ggc gat att cgc ggt att att gaa aag ctg gac 2.407 Asn Asp Asp Gly Ile Gly Asp Ile Arg Gly Ile Ile Glu Lys Leu Asp tat ctg aaa tcg ctc ggt att gac gct atc tgg atc aat ccc cat tac 288. Tyr Leu Lys Ser Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr

	•									•	7 7						
	gac Asp	tct Ser	ccg Pro	aac Asn 100	acc Thr	gat Asp	aac Asn	ggc Gly	tat Tyr 105	gac Asp	atc Ile	agt Ser	aat Asn	tat Tyr 110	cgt Arg	cag Gln	336
	ata Ile	atg Met	aaa Lys 115	gag Glu	tat Tyr	ggc Gly	aca Thr	atg Met 120	gag Glu	gat Asp	ttt Phe	gat Asp	agc Ser 125	ctt Leu	gtt Val	gcc Ala	384
	gaa Glu	atg Met 130	aaa Lys	aaa Lys	cga Arg	aat Asn	atg Met 135	cgc	tta Leu	atg Met	atc Ile	gac Asp 140	gtg Val	gtc Val	att Ile	aac Asn	432
	cat His 145	acc Thr	agt Ser	gat Asp	caa Gln	cac His 150	ccg Pro	tgg Trp	ttt Phe	att Ile	cag Gln 155	agt Ser	aaa Lys	agc Ser	gat Asp	aaa Lys 160	480
	aac Asn	aac Asn	cct Pro	tat Tyr	cgt Arg 165	gac Asp	tat Tyr	tat Tyr	ttc Phe	tgg Trp 170	cgt Arg	gac Asp	gga Gly	aaa Lys	gat Asp 175	aat Asn	528
	cag Gln	cca Pro	cct Pro	aat Asn 180	aat Asn	tac Tyr	ccc Pro	tca Ser	ttt Phe 185	ttc Phe	ggc Gly	ggc Gly	tcg Ser	gca Ala 190	tgg Trp	caa Gln	576
•	aaa Lys	gat Asp	gca Ala 195	aag Lys	tca Ser	gga Gly	Gln	tac Tyr 200	tat Tyr	tta Leu	cac His	tat Tyr	ttt Phe 205	gcc Ala	aga Arg	cag Gln	624
	caa Gln	cct Pro 210	gat Asp	ctc Leu	aac Asn	tgg Trp	gat Asp 215	aac Asn	ccg Pro	aaa Lys	gta Val	cgt Arg 220	gag Glu	gat Asp	ctt Leu	tac Tyr	672
	gca Ala 225	atg Met	ctc Leu	cgc Arg	ttc Phe	tgg Trp 230	ctg Leu	gat Asp	aaa Lys	ggc Gly	gtt Val 235	tca Ser	ggc Gly	atg Met	cga Arg	ttt Phe 240	720
	gat Asp	acg Thr	gtg Val	gca Ala	act Thr 245	tat Tyr	tcc Ser	aaa Lys	atc Ile	ccg Pro 250	gga Gly	ttt Phe	ccc Pro	aat Asn	ctg Leu 255	aca Thr	768
	cct Pro	gaa Glu	caa Gln	cag Gln 260	aaa Lys	aat Asn	ttt Phe	gct Ala	gaa Glu 265	caa Gln	tac Tyr	acc Thr	atg Met	ggg Gly 270	cct Pro	aat Asn	816
	att Ile	cat His	cga Arg 275	tac Tyr	att Ile	cag Gln	gaa Glu	atg Met 280	aac Asn	cgg Arg	aaa Lys	gtt Val	ctg Leu 285	tcc Ser	cgg Arg	tat Tyr	864
	Asp	Val 290	gcc Ala	Thr	Ala	Gly	Glu 295	Ile	Phe	Gly	Val	Pro 300	Leu	Asp	Arg	Ser	912
	tcg Ser 305	cag Gln	ttt Phe	ttt Phe	gat Asp	cgc Arg 310	cgc Arg	cga Arg	cat His	gag Glu	ctg Leu 315	aat Asn	atg Met	gcg Ala	ttt Phe	atg Met 320	960
	ttt Phe	gac Asp	ctc Leu	att Ile	cgt Arg 325	ctc Leu	gat Asp	cgc Arg	gac Asp	agc Ser 330	aat Asn	gaa Glu	cgc Arg	tgg Trp	cgt Arg 335	cac His	1008
	aag Lys	tcg Ser	tgg Trp	tcg Ser 340	ctc Leu	tct Ser	cag Gln	ttc Phe	cgc Arg 345	cag Gln	atc Ile	atc Ile	agċ Ser	aaa Lys 350	átg Met.	gat Asp	1056
	gtc Val	acg Thr	gtc Val 355	gga Gly	aag Lys	tat Tyr	ggc Gly	tgg Trp 360	aac Asn	acg Thr	ttc Phe	ttc Phe	tta Leu 365	gat Asp	aac Asn	cat His	1104

										_							
										GJÀ aaa							1152
										acg Thr							1200
		_	_				_			gag Glu 410	_		_			tat Tyr.	1248
•										gac Asp						ttc Phe	1296
										gtc Val							1344
	_			_	_	_	_	_	_	aac Asn	_	_				_	1392
										act Thr							1440
										aac Asn 490							1488
										aaa Lys							1536
										gcc Ala							1584
										cga Arg							1632
	tat Tyr 545	ctg Leu	gtc Val	gtg Val	gtg Val	aac Asn 550	ttt Phe	aag Lys	gag Glu	tac Tyr	ccg Pro 555	gtc Val	cgc Arg	tat Tyr	act Thr	ctc Leu 560	1680
										gtc Val 570							1728
										tca Ser							1776
		gtg Val					taa			•							1797
	<2·1:1 <2:12)> 18 !> 59 !> PF !> K]	8 RT.	Tella	ı sp.					٠							
)> 18			-												
				Val	Thr 5	Leu	Arg	Thr	Gly	Val 10	Ala	Val	Ala	Leu	Ser 15	Ser	

Leu Ile Ile Ser Leu Ala Cys Pro Ala Val Ser Ala Ala Pro Ser Leu 20 25 Asn Gln Asp Ile His Val Gln Lys Glu Ser Glu Tyr Pro Ala Trp Trp Lys Glu Ala Val Phe Tyr Gln Ile Tyr Pro Arg Ser Phe Lys Asp Thr Asn Asp Asp Gly Ile Gly Asp Ile Arg Gly Ile Ile Glu Lys Leu Asp Tyr Leu Lys Ser Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Ser Asn Tyr Arg Gln 105 Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Ser Leu Val Ala 120 Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn 135 His Thr Ser Asp Gln His Pro Trp Phe Ile Gln Ser Lys Ser Asp Lys 150 155 Asn Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Asn 165 170 Gln Pro Pro Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln 185 Lys Asp Ala Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Arg Gln Gln Pro Asp Leu Asn Trp Asp Asn Pro Lys Val Arg Glu Asp Leu Tyr 215 Ala Met Leu Arg Phe Trp Leu Asp Lys Gly Val Ser Gly Met Arg Phe 225 230 Asp Thr Val Ala Thr Tyr Ser Lys Ile Pro Gly Phe Pro Asn Leu Thr 250 Pro Glu Gln Gln Lys Asn Phe Ala Glu Gln Tyr Thr Met Gly Pro Asn 265 Ile His Arg Tyr Ile Gln Glu Met Asn Arg Lys Val Leu Ser Arg Tyr Asp Val Ala Thr Ala Gly Glu Ile Phe Gly Val Pro Leu Asp Arg Ser 295 300 Ser Gln Phe Phe Asp Arg Arg His Glu Leu Asn Met Ala Phe Met. 315 Phe Asp Leu Ile Arg Leu Asp Arg Asp Ser Asn Glu Arg Trp Arg His 325 Lys Ser Trp Ser Leu Ser Gln Phe Arg Gln Ile Ile Ser Lys Met Asp 345 Val Thr Val Gly Lys Tyr Gly Trp Asn Thr. Phe Phe Leu Asp Asn His 360 Asp Asn Pro Arg Ala Val Ser His Phe Gly Asp Asp Arg Pro Gln Trp. Arg Glu Ala Ser Ala Lys Ala Leu Ala: Thr Ile Thr. Leu. Thr Gln Arg; 390 395

Ala Thr Pro Phe Ile Tyr Gln Gly Ser Glu Leu Gly Met Thr Asn Tyr Pro Phe Arg Gln Leu Asn Glu Phe Asp Asp Ile Glu Val Lys Gly Phe 425 Trp Gln Asp Tyr Val Gln Ser Gly Lys Val Thr Ala Thr Glu Phe Leu Asp Asn Val Arg Leu Thr Ser Arg Asp Asn Ser Arg Thr Pro Phe Gln 455 Trp Asn Asp Thr Leu Asn Ala Gly Phe Thr Arg Gly Lys Pro Trp Phe 470 His Ile Asn Pro Asn Tyr Val Glu Ile Asn Ala Glu Arg Glu Glu Thr 490 Arg Glu Asp Ser Val Leu Asn Tyr Tyr Lys Lys Met Ile Gln Leu Arg 500 505 His His Ile Pro Ala Leu Val Tyr Gly Ala Tyr Gln Asp Leu Asn Pro 520 Gln Asp Asn Thr Val Tyr Ala Tyr Thr Arg Thr Leu Gly Asn Glu Arg 530 Tyr Leu Val Val Val Asn Phe Lys Glu Tyr Pro Val Arg Tyr Thr Leu 545 550 555 Pro Ala Asn Asp Ala Ile Glu Glu Val Val Ile Asp Thr Gln Gln Gln 570 Ala Ala Pro His Ser Thr Ser Leu Ser Leu Ser Pro Trp Gln Ala . 580 585 590 Gly Val Tyr Lys Leu Arg 595 <210> 19. <211> 471 <212> DNA <213> Enterobacter sp. <220> <221> CDS <222> (1)..(471) <223> coding for fragment of sucrose isomerase gtt ttt tat cag atc tat cct cgc tca ttt aaa gac acc aat gat gat Val Phe Tyr Gln Ile Tyr Pro Arg Ser Phe Lys Asp Thr Asn Asp Asp ggc att ggc gat att cgc ggt att att gaa aag ctg gac tat ctg aaa 96 Gly Ile Gly Asp Ile Arg Gly Ile Ile Glu Lys Leu Asp Tyr Leu Lys 20 25 tcg ctc ggt att gac gct atc tgg atc aat ccc cat tac gac tct ccg 144 Ser Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr Asp Ser Pro aac acc gat aac ggc tat gac atc agt aat tat cgt cag ata atg aaa 192. Asn Thr Asp Asn Gly Tyr Asp Ile Ser Asn Tyr Arg Gln Ile Met Lys gag tat ggc aca atg gag gat ttt gat agc ctt gtt gcc gaa atg, aaa Glu Tyr Gly Thr Met Glu Asp Phe Asp Ser Leu Val Ala Glu Met Lys

aaa cga aat atg cgc tta atg atc gac gtg gtc att aac cat acc agt Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn His Thr Ser 85 gat caa cac ccg tgg ttt att cag agt aaa agc gat aaa aac aac cct 336 Asp Gln His Pro Trp Phe Ile Gln Ser Lys Ser Asp Lys Asn Asn Pro 100 105 tat cgt gac tat tat ttc tgg cgt gac gga aaa gat aat cag cca cct 384 Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Asn Gln Pro Pro 115 120 aat aat tac ccc tca ttt ttc ggc ggc tcg gca tgg caa aaa gat gca 432 Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln Lys Asp Ala 135 aag tca gga cag tac tat tta cac tat ttt gcc aga cag 471 Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Arg Gln 145 150 155 <210> 20 <211> 157 <212> PRT <213> Enterobacter sp. <400> 20 Val Phe Tyr Gln Ile Tyr Pro Arg Ser Phe Lys Asp Thr Asn Asp Asp Gly Ile Gly Asp Ile Arg Gly Ile Ile Glu Lys Leu Asp Tyr Leu Lys Ser Leu Gly Ile Asp Ala Ile Trp Ile Asn Pro His Tyr Asp Ser Pro Asn Thr Asp Asn Gly Tyr Asp Ile Ser Asn Tyr Arg Gln Ile Met Lys Glu Tyr Gly Thr Met Glu Asp Phe Asp Ser Leu Val Ala Glu Met Lys Lys Arg Asn Met Arg Leu Met Ile Asp Val Val Ile Asn His Thr Ser Asp Gln His Pro Trp Phe Ile Gln Ser Lys Ser Asp Lys Asn Asn Pro Tyr Arg Asp Tyr Tyr Phe Trp Arg Asp Gly Lys Asp Asn Gln Pro Pro 115 120 Asn Asn Tyr Pro Ser Phe Phe Gly Gly Ser Ala Trp Gln Lys Asp Ala 130 Lys Ser Gly Gln Tyr Tyr Leu His Tyr Phe Ala Arg Gln 145 150 <210> 21 <211> 1782 <212> DNA <213> Pseudomonas mesoacidophila MX45 <220> <221> CDS <222> (1) - . (1779) <223> coding for sucrose isomerase <40.0> 21

atg ctt atg aag aga tta ttc gcc gcg tct ctg atg ctt gct ttt tca

Met 1	Leu	Met	. Lys	Arg	Leu	Phe	: Ala	Ala	Ser 10		Met	Leu	Ala	Phe 15	Ser	
Ser	Val	Ser	Ser 20	Val	. Arg	Ala	gag Glu	Glu . 25	Ala	Val	Lys	Pro	Gly 30	Ala	Pro	96
Trp	Trp	Lys 35	Ser	Ala	Val	Phe	tat Tyr 40	Gln	Val	Tyr	Pro	Arg 45	Ser	Phe	Lys	144
gat Asp	acc Thr 50	Asn	ggt	gat Asp	ggg Gly	atc Ile 55	ggc	gat Asp	ttc Phe	aa a Lys	gga Gly 60	ctg Leu	acg Thr	gag Glu	aag Lys	192
Leu 65	Asp	Tyr	Leu	Lys	Gly 70	Leu	ggc Gly	Ile	Asp	Ala 75	Ile	Trp	Ile	Asn	Pro 80	240
His	Tyr	Ala	Ser	Pro 85	Asn	Thr	gat Asp	Asn	Gly 90	Tyr	Asp	Ile	Ser	Asp 95	Tyr	288
Arg	Glu	Val	Met 100	Lys	Glu	Tyr	ggg Gly	Thr 105	Met	Glu	Asp	Phe	Asp 110	Arg	Leu	336
Met	Ala	Glu 115	Leu	Lys	Lys	Arg	120	Met	Arg	Leu	Met	Val 125	Asp	Val	Val	384
Ile	Asn 130	His	Ser	Ser	Asp	Gln 135	cac His	Glu	Trp	Phe	Lys 140	Ser	Ser	Arg	Ala	432
145	Lys	Asp	Asn	Pro	Tyr 150	Arg	gac Asp	Tyr	Tyr	Phe 155	Trp	Arg	Asp	Gly	Lys 160	480
Asp	Gly	His	Glu	Pro 165	Asn	Asn	tac Tyr	Pro	Ser. 170	Phe	Phe	Gly	Gly	Ser 175	Ala	528
Trp	Glu	Lys	Asp 180	Pro	Val	Thr	ggg	Gln 185	Tyr	Tyr	Leu	His	Tyr 190	Phe	Gly	57 ₆
Arg	GIN	195	Pro	Asp	Leu	Asn	tgg Trp 200	Asp	Thr	Pro	Lys	Leu 205	Arg	Glu	Glu	624
Leu	210	АТа	Met	Leu	Arg	Phe 215	tgg Trp	Leu	Asp	Lys	Gly 220	Val	Ser	Gly	Met	672
Arg 225	Phe	Asp	Thr	Val	Ala 230	Thr	tac Tyr	Ser	Lys	Thr 235	Pro	Gly	Phe	Pro	Asp 240	720
Leu	Thr	Pro	Glu	Gln 245	Met	Lys	aac Asn:	Phe	Ala 25 0 °	Glu:	Ala	Tyr	Thr	Gln 255	GLY.	768
Pro	Asn	Leu	His 260	Arg	Tyr	Leu	cag Gln	G1u 265	Met.	His	Gľu	Lys	Val 270	Phe	Asp.	816
cat His	tat Tyr	gac Asp 275	gcg Ala	gtc Val	acg Thr	gcc Ala	ggc Gly 280	gaa Glu	atc Ile	ttc Phe-	ggc Gly	gct Ala 285	ccg. Pro	ctc Leu	aat Asn	864.

caa Gln	gtg Val 290	. Pro	g cto Lev	tto Phe	atc lle	gac Asp 295	Ser	cgg Arg	agg Arg	aaa Lys	gag Glu 300	Leu	gat Asp	atg Met	gct Ala	912
ttc Phe 305	Thr	tto Phe	gat Asp	cto Lev	atc Ile 310	Arg	tat Tyr	gat Asp	cgc Arg	gca Ala 315	Leu	gat Asp	cgt Arg	tgg Trp	cat His 320	960
acc Thr	att Ile	ccg Pro	g cgt Arg	acc Thr 325	tta Leu	gcg Ala	gac Asp	ttc Phe	cgt Arg 330	Gln	acg Thr	atc Ile	gat Asp	aag Lys 335	gtc Val	1008
Asp	Ala	Ile	340	Gly	gaa Glu	Tyr	Gly	Trp 345	Asn	Thr	Phe	Phe	Leu 350	Gly	Asn	1056
HIS	Asp	355	Pro	Arg	gcg Ala	Val	Ser 360	His	Phe	Gly	Asp	Asp 365	Arg	Pro	Gln	1104
Trp	370	GLU	Ala	Ser	gcc Ala	Lys 375	Ala	Leu	Ala	Thr	Val 380	Thr	Leu	Thr	Gln	1152
385	GTĀ	Thr	Pro	Phe	atc Ile 390	Phe	Gln	Gly	Asp	Glu 395	Leu	Gly	Met	Thr	Asn 400	1200
TYL	PIO	Pne	гÀг	405	ctg Leu	Gln	Asp	Phe	Asp 410	Asp	Ile	Xaa	Xaa	Xaa 415	Xaa	1248
xaa	хаа	хаа	Xaa 420	Xaa	nnn Xaa	Xaa	Xaa	Xaa 425	Xaa	Xaa	Xaa	Xaa	Xaa 430	Xaa	Xaa	1296
хаа	хаа	xaa 435	Xaa	Xaa	nnn Xaa	Xaa	Xaa 440	Xaa	Xaa	Xaa	Xaa	Val 445	Ala	Leu	Thr	1344
ser	450	Ala	Asn	Ala	cgc Arg	Thr 455	Pro	Phe	Gln	Trp	Asp 460	Asp	Ser	Ala	Asn	1392
465	GIY	Pne	Thr	Inr	ggc Gly 470	Lys	Pro	Trp	Leu	Lys 475	Val	Asn	Pro	Asn	Tyr 480	1440
Thr	GIU	ITE	Asn	Ala 485	gcg Ala	Arg	Glu	Ile	Gly 490	Asp	Pro	Lys	Ser	Val 495	Tyr	1488
ser	Pne	Tyr	Arg 500	Asn	ctg Leu	Ile	Ser	Ile 505	Arg	His	Glu	Thr	Pro 510	Ala	Leu	1536
ser	Thr	515	Ser	Tyr	cgc Arg	Asp	Ile 520	Asp	Pro	Ser	Asn	Ala 525	Asp	Val	Tyr.	1584
Ата	530	Thr	Arg	Ser		Asp 535	Gly	Glu	Thr	Tyr	Leu 540	Val	Val	Val	Asn	1632
ttc Phe 545	aag Lys	gca Ala	gag Glu	cca Pro	agg Arg 550	agt Ser	ttc Phe	acg Thr	ctt Leu	ccg Pro 555	gac Asp	ggc Gly	atg Met	His	att Ile 560	1680

										* _						
														gcg Ala 575		1728
gct Ala	gca Ala	agc Ser	ctt Leu 580	gag Glu	ctg Leu	cag Gln	cct Pro	tgg Trp 585	cag Gln	tcc Ser	ggc Gly	atc Ile	tac Tyr 590	aag Lys	gtg Val	1776
aag Lys	taa											ī				1782
<211 <212)> 2: l> 5! 2> P! 3> P:	93 RT	omona	as me	esoad	cido	phila	a MX4	15							
<400)> 22	2											•			
			Lys	Arg 5	Leu	Phe	Ala	Ala	Ser 10	Leu	Met	Leu	Ala	Phe 15	Ser	
Ser	Val	Ser	Ser 20	Val	Arg	Ala	Glu	Glu 25	Ala	Val	Lys	Pro	Gly 30	Ala	Pro	
Trp	Trp	Lys 35	Ser	Ala	Val	Phe	Tyr 40	Gln	Val	Tyr	Pro	Arg 45	Ser	Phe	Lys	
Asp	Thr 50	Asn	Gly	Asp	Gly	Ile 55	Gly	Asp	Phe	Lys	Gly 60	Leu	Thr	Glu	Lys	
Leu 65	Asp	Tyr	Leu	Lys	Gly 70	Leu	Gly	Ile	Asp	Ala 75	Ilè	Trp	Ile	Asn	Pro 80	
His	Tyr	Ala	Ser	Pro 85	Asn	Thr	Asp	Asn	Gly 90	Tyr	Asp	Ile	Ser	Asp 95	Tyr	ŢŢ.
Arg	Glu	Val	Met 100	Lys	Glu	Tyr	Gly	Thr 105	Met	Glu	Asp	Phe	Asp 110	Arg	Leu	
Met	Ala	Glu 115	Leu	Lys	Lys	Arg	Gly 120	Met	Arg	Leu	Met	Val 125	Asp	Val	Val	
Ile	Asn 130	His	Ser	Ser	Asp	.Gln 135	His	Glu	Trp	Phe	Lys 140	Ser	Ser	Arg	Àla	
145					150					155				Gly	160	
				165					170					Ser 175		
			180					185					190	Phe	_	
		195					200				_	205	- 4	Glu		
	210			•	•	215				•	220			Gly		
225					230					235				Pro	240	
				245					250					Gln 255		
			260.					2.65					270		_	
His	Tyr	Asp 275	Ala	Val	Thr	Ala	Gl <u>y</u> 280	Gľu	Ile	Phe	Gly	Ala 285	Pro	Leu	Asn	

										-					
Gln	Val 290	Pro	Leu	Phe	Ile	Asp 295	Ser	Arg	Arg	Lys	Glu 300	Leu	Asp	Met	Ala
Phe 305	Thr	Phe	Asp	Leu	Ile 310	Arg	Tyr	Asp	Arg	Ala 315	Leu	Asp	Arg	Trp	His 320
Thr	Ile	Pro	Arg	Thr 325	Leu	Ala	Asp	Phe	Arg 330	Gln	Thr	Ile	Asp	Lys 335	Val
Asp	Ala	Ile	Ala 340	Gly	Glu	Tyr	Gly	Trp 345	Asn	Thr	Phe	Phe	Leu 350	Gly	Asn
His	Asp	Asn 355	Pro	Arg	Ala	Val	Ser 360	His	Phe	Gly	Asp	Asp 365	Arg	Pro	Gln
Trp	Arg 370	Glu	Ala	Ser	Ala	Lys 375	Ala	Leu	Ala	Thr	Val 380	Thr	Leu	Thr	Gln
Arg 385	Gly	Thr	Pro	Phe	Ile 390	Phe	Gln	Gly	Asp	Glu 395	Leu	Gly	Met	Thr	Asn 400
Tyr	Pro	Phe	Lys	Thr 405	Leu	Gln	Asp		Asp 410	Asp	Ile	Xaa	Xaa	Xaa 415	Xaa
Xaa	Xaa	Xaa	Xaa 420	Xaa	Xaa	Xaa	Xaa	Xaa 425	.Xáa	Xaa	Xaa	Xaa	Xa'a 430	Xaa	Xaa
Xaa	Xaa	Xaa 435	Xaa	Xaa	Xaa	Xaa	Xaa 440	Xaa	Xaa	Xaa	Xaa	Val 445	Ala	Leu	Thr
Ser	Arg 450	Ala	Asn	Ala	Arg	Thr 455	Pro	Phe	Gln	Ţrp	Asp 460	Asp	Ser	Ala	Asn
465.	_	•	Thr	•	470	_				475					480
Thr	Glu	Ile	Asn	Ala 485	Ala	Arg	Glu	Ile	Gly 490	Asp	Pro	Lys	Ser	Val 495	Tyr
			Arg 500					505	_		•		510		
Ser	Thr	Gly 515	Ser	Tyr	Arg	Asp	Ile 520	Asp	Pro	Ser	Asn	Ala 525	Asp	Val	Tyr
	5.30		Arg			535				_	540				•
Phe 545	Lys	Ala	Glu	Pro	Arg 550	Ser	Phe	Thr	Leu	Pro 555	Asp	Gly	Met	His	Ile 560
Ala	Glu	Thr	Leu	Ile 565	Glu	Ser	Ser	Ser	Pro 570	Ala	Ala	Pro	Ala	Ala 575	Gly
Ala	Ala	Ser	Leu 580	Glu	Leu	Gln	Pro	Trp 585	Gln	Ser	Gly	Ile	Tyr 590	Lys	Val

Lys

<210> 23

<211> 1417

<212> DNA

<213> Lycopersicon esculentum.

<220>

<221> promoter <222> (1)...(1417) <223> promoter of lemmi9

```
<400> 23
ataatttaac catctagaga tccacaaatc atgtttccat atcatggtag tagttggtgc 60
tacgaagtat ctataaatta ttgagaaata cctggtggaa tcccaagtga aacggaaagg 120
cccttactta ttaaataaaa aaacatttga caatagaaaa ttgagaccaa tctgcatatg 180
aaacatcagg atccccacat ttcacaaatt ttacaagtta attaagccct actctgtcca 240
tatggaactt ttctgcactt ccacgcacca acgaatatgc tgaaaattga tgttttagat 300
gtgtacgaat aaagcaatca aagaacgcgg gcgcaacgcg cgctggagac actgccattc 360
atgtgtgcct aacgtgtttt ctttagtcat tacgctccta ctaccgactc aatatatatt 420
aactatagta ttttttattt atgacgagaa acgtaatttt aaatgtagat atattttaac 480
aagctatgat aattacatct tgttgccgta gtcataaatg acacaaatta aggtttgatt 540
ttcgtccact tctaagattt cttgttctaa tactagtata tttctgattt aaaaagttat 600
ttagtttttt ttgaattagc tgataaatgc caaaaactga aaattaaagt actttttaat 660
tttataaaaa taatatcatg gaaattaaaa cgagaaatta atgaaaaagt agaagattgc 720
tttgccataa tatagtgtta cttttcgtat tattttatta agcgtaaaat tacataaagg 780
tatccgtgct taaatttcta gcttgagagc attttttgaa gcaaaagttt cgataaatca 840
agttttaata taaaattaca atcatcattt ctaattatat taattcttta aaaataaaat 900
taaaaaaata tatacaataa ttgaagctcg gataaattaa aatatgtaac tattaaatat 960
tactcggata tattaaatat tattcgatta tattaatatg tagctcaaaa tatattaaat 1020
aataatacaa atatattaat atatgtaaat catatacatt aaaaactatc ttaaatatat 1080
aatatgcagc tgtaatatat taacccagat acataagcac ctcgagtaca ttaaacaaat 1140
aaaagaattt aaaaataata aaaataagtg aaagcaataa attgtatatt tctataattt 1200
atccctttat taatactaaa taaagttaga gaacctaaac aggaagcaca attatgacac 1260
gaggagagaa tagcgcgtca attgtgaccc tttacgcgga agtatatgta ataaatagta 1320
gactcttttt ctatatttgt atatcccata acaagagcag agatattcgt ttagcacaaa 1380
acaggcatac tattcaattc cctttcgttc cagaagc
<210> 24
<211> 374
<212> DNA
<213> Nicotiana tabacum
<220>
<221> promoter
<222> (1)..(374)
<223> promoter of delta-0.3TobRB7
<400> 24
agcttatcta aacaaagttt taaattcatt tcttaaacgt ccattacaat gtaatataac 60
ttagtcgtct caattaaacc attaatgtga aatataaatc aaaaaaagcc aaagggcggt 120
gggacggcgc caatcatttg tcctagtcca ctcaaataag gcccatggtc ggcaaaacca 180
aacacaaaat gtgttatttt taattttttc ctcttttatt gttaaagttg caaaatgtgt 240
tatttttggt aagaccctat ggatatataa agacaggtta tgtgaaactt ggaaaaccat 300
caagttttaa gcaaaaccct cttaagaact taaattgagc ttcttttggg gcatttttct 360
agtgagaact aaaa
                                                                   374
<210> 25
<211> 27
<212> DNA
<213> Artificial sequence
<220>
<223> Description of the artificial sequence:
      oligonucleotide primer
<400> 25
ggatccggta ccgttcagca atcaaat
                                                                   27
<210> 26
<211> 23
<212> DNA
<213> Artificial sequence
```

<220> <223>	Description of the artificial sequence:	
	oligonucleotide primer	
<400> gtcgad	26 Egtct tgccaaaac ctt	23
<210><211><212><213>	25	
<220> <223>	Description of the artificial sequence: oligonucleotide primer	
<400>	27	
gtcgac	cctac gtgattaagt ttata	25
<210><211><212><213>	28	
<220> <223>	Description of the artificial sequence: oligonucleotide primer	
<400>		
	attca taatttaacc atctagag	28
<210> <211> <212>	29 28 DNA	20
•	Artificial sequence	
	Description of the artificial sequence: oligonucleotide primer	
<400>	29	
atcggt	acct gcttctggaa cgaaaggg	28
<210> <211> <212> <213>	34	
<220>		
<223>	Description of the artificial sequence: oligonucleotide primer	
<400>	·	
	cago ttatotaaac aaagttttaa atto	34
<210> <211> <212> <213>	30	
<220> <223>	Description of the artificial sequence: oligonucleotide primer	
<400>		
	cagt tctcactaga aaaatgcccc	30
<210>- <211>		

45

```
<212> DNA
<213> Wheat dwarf virus
<220>
<221> promoter
<222> (1)..(461)
<223> V-sense promoter from Wheat Dwarf Virus
ccggcaggtc cttagcgaaa aaacggggtg tgccagaaaa ctctatgctc taccctgcgt 60
ggaggtgtga attctgcaca ctgctaatgc aatgtgtcca atgctttata tagggcaggt 120
tttggcggga gaacagggcc cttgtgttcc cacgggagcg tagcgtatcg tgtgggcct 180
gttcggtgtg tggtcggggg gcctccacgc gggttataat attaccccgc gtggtggccc 240
ccgacgcgca ctcggctttt cgtgagtgcg cggaggcttt tggaccacat cttttctgac 300
cactttcgtg gaatatgttg atttatcaca cttttgacgc ggaaatctgt gccatgcctt 360
agettataag gaagtgegtg gtageeeate tegatggage aggeaatage ecceeegett 420
cctatacggg actatcaata ccagacccct tccattcccg g
<210> 33
<211> 1173
<212> DNA
<213> Maize streak virus
<220>
<221> promoter
<222> (1)..(1173)
<223> V-sense promotor from Maize Streak Virus
<400> 33
aagcttattt gcagagtatt caaaatactg caattttgtg gaccaatcaa agggaagctc 60
tttctggatc atggagaggt actcttcttt ggaagtagcg tgtgaaataa tgtctcgcat 120
tatttcatct ttagaaggct tttttcctt tacctctgaa tcagattttc cgaggaaggg 180
ggacttccta ggaatgaaag tacctctctc aaacacagcc agaggttcct tgagaatgta 240
atccctcacc ctgtttactg acttggcact ctgaatattt gggtgaaacc catttatatc 300
aaagaacctt gagtcagata tccttaccgg cttctctgtc tgaagcaatg catgtaaatg 360
caaacttcca tctttatgtg cctctcgggc acatagaatg tatttgggaa tccaacgaac 420
aacgagctcc cagatcatct gacaggcgat ttcaggattt tctggacact ttggataggt 480
taggaacgtg ttagcgttcc ggtgtgagaa ctgacggttg gatgaggagg aggccattgc 540
cgacgacgga ggttgaggct gagggatggc agactgggag ctccaaactc tatagtatac 600
ccgtgcgcct tcgcctcgag gcgaaatccg ccgctccctt gtcttgtagt ggttgcaaat 660
gggccggacc gggccggccc agcaggaaaa gaaggcgcgc actaatatta ccgcgccttc 720
ttttcctgcg agggcccggt agggtcgacc ccgagcgatt tgatgtaaag tttggtcctg 780
ctttgtatga tttatctaaa gcagcccatt ctaaagaatc cggtcccggt cactataaat 840
tgcctaacaa gtgcgattca ttcatggatc cacagaacgc cctgtattat cagccgcggg 900
tacccacage ageteegaca teeggaggag tgeegtggag tegegtagge gaggtageta 960
ttttgagctt tgttgcattg atttgctttt acctgcttta cctttgggtg ctgagagacc 1020
ttatcttagt tctgaaggct cgacaaggca gatccacgga ggagctgata tttggtggac 1080
aagctgtgga taggagcaac cctatcccta atataccagc accaccaagt cagggcaatc 1140
ccgggccatt tgttccatcg actctagtcg acc
<210> 34
<211> 353
<212> DNA
<213> Pepper huasteco virus
<220>
<221> promoter
<222> (1)...(353)
<223> V-sense promoter from Pepper huasteco virus
<400> 34
catatttgta ataagagagg tgtacaccga ttggagctct ttaacctggg cttattgtat 60
cggtgtattg gtagccaata tatagtatat gggagttatc taggatcttc gtacacgtga 120°
```

tta tag ttt <21 <21	tttg ttat	aat cag att 5 803	taaa ttcc	gatg agac	tt a gt g	cttt ggga	tatg	c ta g ta	tcca gtgt	atg <mark>a</mark> atga	agc cca	gtag cttt	cgt att	ctgg gact	actgct gaagct gtcagc	240
		erra	tia	plym	uthi	ca										
<22	1>.C 2> (1)			cros	e is	omer	ase								
	0> 3	-														,
Met 1	Pro	Arg	Gln	gga Gly 5	ttg Leu	aaa Lys	act Thr	gca Ala	cta Leu 10	gcg Ala	att Ile	ttt Phe	cta Leu	acc Thr 15	aca Thr	48
tca Ser	tta Leu	agc Ser	gtc Val 20	tca Ser	tgc Cys	cag Gln	caa Gln	gcc Ala 25	tta Leu	ggt Gly	acg Thr	caa Gln	caa Gln 30	ccc Pro	ttg Leu	96
ctt Leu	aac Asn	gaa Glu 35	aag Lys	agt Ser	atc Ile	gaa Glu	cag Gln 40	tcg Ser	aaa Lys	acc	ata Ile	cct Pro 45	aaa Lys	tgg Trp	tgg Trp	144
aag Lys	gag Glu 50	gct Ala	gtt Val	ttt Phe	tat Tyr	cag Gln 55	gtg Val	tat Tyr	ccg Pro	cgt Arg	tcc Ser 60	ttt Phe	aaa Lys	gac Asp	act Thr	192
aac Asn 65	ggg Gly	gat Asp	ggt Gly	atc Ile	999 Gly 70	gat Asp	att Ile	aaa Lys	ggc Gly	atc Ile 75	ata Ile	gaa Glu	aaa Lys	tta Leu	gac Asp 80	240
tat Tyr	tta Leu	aaa Lys	gct Ala	ttg Leu 85	ggg Gly	att Ile	gat Asp	gcc Ala	att Ile 90	tgg Trp	atc Ile	aac Asn	cca Pro	cat His 95	tat Tyr	288
gac Asp	tcc Ser	ccg Pro	aac Asn 100	acg Thr	gat Asp	aat Asn	ggt Gly	tac Tyr 105	gat Asp	ata Ile	cgt Arg	gat Asp	tat Tyr 110	cga Arg	aaa Lys	336
atc Ile	atg Met	aaa Lys 115	gaa Glu	tat Tyr	ggc	acg Thr	atg Met 120	gag Glu	gat	ttt Phe	gac Asp	cgc Arg 125	ctg Leu	att Ile	tct Ser	384
gaa Glu	atg Met 130	aaa Lys	aaa Lys	cgt Arg	aac Asn	atg Met 135	cgg Arg	ttg Leu	atg Met	att Ile	gat Asp 140	gtg Val	gtc Val	atc Ile	aac Asn	432
cac His 145	acc Thr	agc Ser	gat Asp	caa Gln	aac Asn 150	gaa Glu	tgg Trp	ttt Phe	gtt Val	aaa Lys 155	agt Ser	aaa Lys	agc Ser	agt Ser	aag Lys 160	480
gat Asp	aat Asn	cct Pro	tat Tyr	cgt Arg 165	ggc Gly	tat Tyr	tac Tyr	ttc Phe	tgg Trp 170	aaa Lys	gat Asp	gct Ala	aaa Lys	gaa Gľu 175	elå aaa	528
cag Gln	gcg Ala	cct Pro	aat Asn 180	aat Asn	tac Tyr	cct Pro	tca Ser	ttc Phe 185	ttt. Phe	ggt Gly	ggc Gly	tcg Ser	gcg Ala 190	tgg. Trp	caa Gln	576:
aaa Lys	gat Asp	gaa Glu 195	aag Lys	acc Thr	aat Asn	caa Gln	tac Tyr 200	tac Tyr	ctg Leu	cac His	tat Tyr	ttt Phe 205	gct Ala	aaa Lys	caa. Gln	624

									•	- ,					•	
					tgg Trp											672
gca Ala 225	atg Met	ttg Leu	cgt Arg	ttc Phe	tgg Trp 230	tta Leu	gat Asp	aaa Lys	ggc Gly	gtg Val 235	tct Ser	ggt Gly	tta Leu	cgc Arg	ttt Phe 240	720
					tac Tyr											768
					aat Asn											816
					aat Asn											864
					ggt Gly											912
ata Ile 305	aaa Lys	ttc Phe	ttc Phe	gat Asp	cgc Arg 310	cgt Arg	cgc Arg	gat Asp	gag Glu	ctg Leu 315	aac Asn	atc Ile	gca Ala	ttt Phe	acc Thr 320	960
					ctc Leu											1008
					tcg Ser											1056
			Gly		tat Tyr											1104
gac Asp	aat Asn 370	ccg Pro	cgc Arg	gct Ala	gtc Val	tcc Ser 375	cac His	ttt Phe	ggc Gly	gat Asp	gat Asp 380	cgc Arg	cca Pro	caa Gln	tgg Trp	1152
cgc Arg 385	gag Glu	cca Pro	tcg Ser	gct Ala	aaa Lys 390	gcg Ala	ctt Leu	gca Ala	acc Thr	ttg Leu 395	acg Thr	ctg Leu	act Thr	caa Gln	cga Arg 400	1200
gca Ala	acg Thr	cct Pro	ttt Phe	att Ile 405	tat Tyr	caa Gln	ggt Gly	tca Ser	gaa Glu 410	ttg Leu	ggc Gly	atg Met	acc Thr	aat Asn 415	tac Tyr	1248
ccc Pro	ttc Phe	aaa Lys	gct Ala 420	att Ile	gat Asp	gaa Glu	ttc Phe	gat Asp 425	gat Asp	att Ile	gag Glu	gtg Val	aaa Lys 430	ggt Gly	ttt Phe	1296
tgg Trp	cat His	gac Asp 435	tac Tyr	gtt Val	gag Glu	aca Thr	gga Gly 440	aag Lys	gtg Val	aaa Lys	gcc Ala	gac Asp 445	gag Glu	ttc Phe	ttg Leu	1344
caa Gln	aat Asn 450	gta Val	cgc Arg	ctg Leu	acg Thr	agc Ser 455	agg Ar g	gat Asp	aac Asn	agc Ser	cgg Arg 460	aca Thr	ccg Pro	ttc Phe	caa Gln	1392
tgg Trp 465	gat Asp	acg Thr	agc Ser	aaa Lys	aat Asn 470	gca Aľa	gga Gly	ttc Phe	acg Thr	agc Ser 475	gga Gly	aaa Lys	cct Pro	tgg Trp	ttc Phe 480	1440

									-							
aag .Lys	gtc Val	aat Asn	cca Pro	aac Asn 485	tac Tyr	cag Gln	gaa Glu	atc Ile	aat Asn 490	gcg Ala	gta Val	agt Ser	caa Gln	gtc Val 495	gca Ala	1488
cag Gln	ccc Pro	gac Asp	tcg Ser 500	gta Val	ttt Phe	aat Asn	tat Tyr	tat Tyr 505	cgt Arg	cag Gln	ttg Leu	atc Ile	aag Lys 510	ata Ile	agg Arg	1536
					ctg Leu											1584
gca Ala	aat Asn 530	gat Asp	tcg Ser	gtc Val	tac Tyr	gcc Ala 535	tat Tyr	aca Thr	cgc Arg	agc Ser	ctt Leu 540	ggg Gly	gcg Ala	gaa Glu	aaa Lys	1632
					aac Asn 550											1680
ccg Pro	gat Asp	aat Asn	cta Leu	tcc Ser 565	atc Ile	gag Glu	aaa Lys	gtg Val	att Ile 570	ata Ile	gaa Glu	agc Ser	aac Asn	agc Ser 575	aaa Lys	1728
				Lys	aat Asn				Leu							1776
					cta Leu			taa	•					•		1803
<210)> 36	5					•									
	1 ~ 61	١٨														
<213																
<212	2> PI	RТ	tia m	olvmı	ıthio	ca										•
<212 <213	2> PI 3> Se	RT errat	tia p	ρlymι	ıthio	ca										•
<212 <213 <400 Met	2> PI 3> Se 0> 36 Pro	RT errat 5 Arg	Gln	Gly 5	Leu	Lys			10					15		٠
<212 <213 <400 Met	2> PI 3> Se 0> 36 Pro	RT errat 5 Arg	Gln	Gly 5		Lys			10					15		•
<212 <213 <400 Met 1 Ser	2> PF 3> Se 0> 36 Pro Leu	RT errat 6 Arg Ser	Gln Val 20 Lys	Gly 5 Ser	Leu Cys	Lys Gln	Gln Gln	Ala 25 Ser	10 Leu	Gly	Thr	Gln	Gln 30 Lys	15 Pro	Leu	
<213 <213 <400 Met 1 Ser	2> PF 3> Se 0> 36 Pro Leu	RT errat 5 Arg Ser Glu 35	Gln Val 20 Lys	Gly 5 Ser	Leu Cys	Lys Gln Glu	Gln Gln 40	Ala 25 Ser	10 Leu Lys	Gly Thr	Thr	Gln Pro 45	Gln 30 Lys	15 Pro Trp	Leu Trp	
<213 <213 <400 Met 1 Ser Leu	2> PF 3> Se Pro Leu Asn Glu 50	RT errat S Arg Ser Glu 35 Ala	Gln Val 20 Lys Val	Gly 5 Ser Ser	Leu Cys Ile	Lys Gln Glu Gln 55	Gln Gln 40 Val	Ala 25 Ser Tyr	10 Leu Lys Pro	Gly Thr Arg	Thr Ile Ser 60	Gln Pro 45 Phe	Gln 30 Lys Lys	15 Pro Trp Asp	Leu Trp Thr	
<212 <213 <400 Met 1 Ser Leu Lys Asn 65	2> PF 3> Se 0> 36 Pro Leu Asn Glu 50 Gly	RT errate Ser Ser Glu 35 Ala	Gln Val 20 Lys Val Gly	Gly 5 Ser Ser	Leu Cys Ile Tyr	Lys Gln Glu Gln 55 Asp	Gln Gln 40 Val	Ala 25 Ser Tyr	10 Leu Lys Pro Gly	Gly Thr Arg Ile 75	Thr Ile Ser 60 Ile	Gln Pro 45 Phe Glu	Gln 30 Lys Lys	15 Pro Trp Asp Leu	Leu Trp Thr Asp 80	
<213 <400 Met 1 Ser Leu Lys Asn 65 Tyr	2> PP 3> Se Pro Leu Asn Glu 50 Gly Leu	RT errate Ser Ser Glu 35 Ala Asp	Gln Val 20 Lys Val Gly	Gly 5 Ser Ser Phe Ile Leu 85	Leu Cys Ile Tyr Gly	Lys Gln Glu Gln 55 Asp	Gln 40 Val Ile Asp	Ala 25 Ser Tyr Lys Ala	10 Leu Lys Pro Gly Ile 90	Gly Thr Arg Ile 75 Trp	Thr Ile Ser 60 Ile Ile	Gln Pro 45 Phe Glu Asn	Gln 30 Lys Lys Lys	15 Pro Trp Asp Leu His 95	Leu Trp Thr Asp 80 Tyr	
<212 <400 Met 1 Ser Leu Lys Asn 65 Tyr	2> PP 3> Se 0> 36 Pro Leu Asn Glu 50 Gly Leu Ser	RT errate Ser Ser Glu 35 Ala Asp Lys	Gln Val 20 Lys Val Gly Ala Asn 100	Gly 5 Ser Ser Phe Ile Leu 85 Thr	Leu Cys Ile Tyr Gly 70	Lys Gln Glu Gln 55 Asp Ile Asn	Gln 40 Val Ile Asp Gly	Ala 25 Ser Tyr Lys Ala Tyr 105	Lys Pro Gly Ile 90 Asp	Gly Thr Arg Ile 75 Trp Ile	Thr Ile Ser 60 Ile Ile Arg	Gln Pro 45 Phe Glu Asn Asp	Gln 30 Lys Lys Lys Pro	15 Pro Trp Asp Leu His 95 Arg	Leu Trp Thr Asp 80 Tyr Lys	
<213 <400 Met 1 Ser Leu Lys Asn 655 Tyr Asp	2> PR 3> Se 2> 30 Pro Leu Asn Glu 50 Gly Leu Ser Met	Ser Glu 35 Ala Asp Lys Pro Lys 115	Gln Val 20 Lys Val Gly Ala Asn 100 Glu	Gly 5 Ser Ser Phe Ile Leu 85 Thr	Leu Cys Ile Tyr Gly 70 Gly Asp	Lys Gln Glu Gln 55 Asp Ile Asn	Gln 40 Val Ile Asp Gly Met 120	Ala 25 Ser Tyr Lys Ala Tyr 105 Glu	10 Leu Lys Pro Gly Ile 90 Asp	Gly Thr Arg Ile 75 Trp Ile Phe	Thr Ile Ser 60 Ile Ile Arg	Gln Pro 45 Phe Glu Asn Asp Arg 125	Gln 30 Lys Lys Pro Tyr 110 Leu	15 Pro Trp Asp Leu His 95 Arg	Leu Trp Thr Asp 80 Tyr Lys Ser	
<213 <400 Met 1 Ser Leu Lys Asn 65 Tyr Asp Ile Glu	2> PR 3> Se 2> 30 Pro Leu Asn Glu 50 Gly Leu Ser Met	Ser Glu 35 Ala Asp Lys Pro Lys 115 Lys	Gln Val 20 Lys Val Gly Ala Asn 100 Glu Lys	Gly 5 Ser Ser Phe Ile 185 Thr Tyr Arg	Leu Cys Ile Tyr Gly 70 Gly Asp	Lys Gln Glu Gln 55 Asp Ile Asn Thr	Gln 40 Val Ile Asp Gly Met 120 Arg	Ala 25 Ser Tyr Lys Ala Tyr 105 Glu Leu	10 Leu Lys Pro Gly Ile 90 Asp Asp	Gly Thr Arg Ile 75 Trp Ile Phe Ile	Thr Ile Ser 60 Ile Ile Arg Asp Asp 140	Gln Pro 45 Phe Glu Asn Asp Arg 125 Val	Gln 30 Lys Lys Lys Pro Tyr 110 Leu	15 Pro Trp Asp Leu His 95 Arg Ile	Leu Trp Thr Asp 80 Tyr Lys Ser Asn	

										49					
Glı	n Ala	a Pro	180	n Ası O	n Tyr	Pro	Ser	Phe 185		Gly	Gly	Ser	Ala 190		Gln
Lys	s Asp	Gl:	ı Ly: 5	s Thi	. Asn	Gln	Tyr 200	Tyr	Leu	His	Tyr	Phe 205		Lys	Gln
Gl	210	Asp)) Lei	u Ası	1 Trp	Asp 215	Asn	Pro	Lys	Val	Arg 220		Asp	Ļeu	Tyr
Ala 225	a Met	: Let	ı Arç	g Phe	230	Leu	Asp	Lys	Gly	Val 235		Gly	Leu	Arg	Phe 240
Asp	Thr	: Val	L Ala	245	Tyr	Ser	Lys	Ile	Pro 250	Asp	Phe	Pro	Asn	Leu 255	
Glr	Gln	Glr	Let 260	Lys)	Asn	Phe	Ala	Ala 265	Glu	Tyr	Thr	Lys	Gly 270		Asn
		275	•		. Asn		280					285			-
	290				Gly	295					300				
Ile 305	Lys	Phe	Phe	Asp	Arg 310	Arg	Arg	Asp	Glu	Leu 315	Asn	Ile	Ala	Phe	Thr 320
				325					330					335	_
			340		Ser			345					350		_
	•	355			Tyr		360					365			
	3/0				Val	375					380				
385					Lys 390					395					400
		•		405	Tyr				410					415	
	•		420		Asp			425					430		
		435			Glu		440					445			
	450		,		Thr	455					460				
465					Asn 470					475					480
				485	Tyr			٠	490					495	
			500		Phe			505					510		
		515			Leu		520					525			
	530					535					540				
Tyr 545	Leu	Val	Val	Val	Asn´: 550	Phe	Gln	Glu		Val. 555	Met	Arg	Tyr	Lys	Leu 560

50

Pro Asp Asn Leu Ser Ile Glu Lys Val Ile Ile Glu Ser Asn Ser Lys 565 570 575

Asn Val Val Lys Lys Asn Asp Ser Leu Leu Glu Leu Lys Pro Trp Gln 580 590

Ser Gly Val Tyr Lys Leu Asn Gln 595 600